



SEQUENCE LISTING

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<120> Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same

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<141> 2000-09-18

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<151> 2000-02-22

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<151> 1999-07-07

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<213> Homo sapiens

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```

Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro Cys His
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```

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Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
      35              40              45

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```

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
      50              55              60

```

```

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
      65              70              75              80

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```

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
      85              90              95

```

```

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
      100             105             110

```

```

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
      115             120             125

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```

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
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```

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
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Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
      165             170             175

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Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
      180             185             190

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His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
      195             200             205

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Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
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 Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
 225 230 235 240
 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
 245 250 255
 Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
 260 265 270
 Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
 275 280 285
 Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys
 290 295 300
 Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
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Leu

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 <212> DNA
 <213> Homo sapiens

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<210> 4

<211> 379

<212> PRT

<213> Homo sapiens

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Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln
      20                      25                      30

```

```

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
      35                      40                      45

```

```

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
      50                      55                      60

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Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
      65                      70                      75                      80

```

```

Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
      85                      90                      95

```

```

Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
      100                      105                      110

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```

Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
      115                      120                      125

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```

His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
      130                      135                      140

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```

Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu
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```

Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
      165                      170                      175

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Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
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 Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His
 195 200 205
 Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220
 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240
 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255
 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
 260 265 270
 Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285
 Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu
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 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320
 His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His
 325 330 335
 Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala
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<210> 5

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<210> 8

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<210> 9

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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<210> 10

<211> 23

<212> DNA

<213> Artificial Sequence

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oligonucleotide probe

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<210> 11

<211> 2197

<212> DNA

<213> Homo sapiens

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<210> 12

<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

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```

```
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      20                      25                      30
```

```
Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
      35                      40                      45
```

```
Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
```


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Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro		
	85	90 95
Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr		
	100	105 110
Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln		
	115	120 125
Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln		
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Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly		
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His Asp Pro Gly

<210> 13
 <211> 533
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 <213> Homo sapiens

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 <223> a, t, c or g

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<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 14
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<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide probe

<400> 15
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<210> 16
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<210> 17
<211> 960
<212> DNA
<213> Homo sapiens

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<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

<400> 18

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Met Thr His Arg Thr Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val
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      20              25              30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
      35              40              45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
      50              55              60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
      65              70              75              80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
      85              90              95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
      100             105             110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
      115             120             125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
      130             135             140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
      145             150             155             160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
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Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
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<210> 19

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 19
tgctgtgcta ctcctgcaaa gccc 24

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 20
tgcacaagtc ggtgtcacag cacg 24

<210> 21
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 21
agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg 44

<210> 22
<211> 1200
<212> DNA
<213> Homo sapiens

<400> 22
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<400> 23
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          20          25          30
Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
          35          40          45
Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
          50          55          60
Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
  65          70          75          80
Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
          85          90          95
Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
          100          105          110
Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
          115          120          125
Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
          130          135          140
Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
  145          150          155          160
Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
          165          170          175
His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr
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<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 24

cagtacgtga gggaccaggg cgccatga

28

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 25

ccggtgacct gcacgtgctt gcca

24

<210> 26

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<220>

<221> modified_base

<222> (21)..(21)

<223> a, t, c or g

<400> 26

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41

<210> 27

<211> 2479

<212> DNA

<213> Homo sapiens

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2479

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<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

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Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
      20              25              30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
      35              40              45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
      50              55              60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
      65              70              75              80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
      85              90              95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
      100             105             110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
      115             120             125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser

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Gly	Leu	Pro	Val	Asp	Leu	Gln	Glu	Leu	Arg	Val	Asp	Glu	Asn	Arg	Ile
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Ala	Val	Ile	Ser	Asp	Met	Ala	Phe	Gln	Asn	Leu	Thr	Ser	Leu	Glu	Arg
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Leu	Thr	Ala	Arg	Asn	Asn	Pro	Trp	Phe	Cys	Asp	Cys	Ser	Ile	Lys	Trp
305						310				315					320
Val	Thr	Glu	Trp	Leu	Lys	Tyr	Ile	Pro	Ser	Ser	Leu	Asn	Val	Arg	Gly
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Phe	Met	Cys	Gln	Gly	Pro	Glu	Gln	Val	Arg	Gly	Met	Ala	Val	Arg	Glu
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Leu	Asn	Met	Asn	Leu	Leu	Ser	Cys	Pro	Thr	Thr	Thr	Pro	Gly	Leu	Pro
		355					360					365			
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	370					375					380				
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385					390					395					400
Thr	Thr	Ser	Lys	Leu	Pro	Thr	Ile	Pro	Asp	Trp	Asp	Gly	Arg	Glu	Arg
				405					410					415	
Val	Thr	Pro	Pro	Ile	Ser	Glu	Arg	Ile	Gln	Leu	Ser	Ile	His	Phe	Val
			420					425					430		
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465					470					475					480
Val	Asn	Leu	Glu	Pro	Arg	Ser	Thr	Tyr	Arg	Ile	Cys	Leu	Val	Pro	Leu
				485					490					495	
Asp	Ala	Phe	Asn	Tyr	Arg	Ala	Val	Glu	Asp	Thr	Ile	Cys	Ser	Glu	Ala
			500					505					510		
Thr	Thr	His	Ala	Ser	Tyr	Leu	Asn	Asn	Gly	Ser	Asn	Thr	Ala	Ser	Ser
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Val	Phe	Cys	Trp	His	Met	His	Lys	Lys	Gly	Arg	Tyr	Thr	Ser	Gln	Lys
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Trp	Lys	Tyr	Asn	Arg	Gly	Arg	Arg	Lys	Asp	Asp	Tyr	Cys	Glu	Ala	Gly
			580					585					590		
Thr	Lys	Lys	Asp	Asn	Ser	Ile	Leu	Glu	Met	Thr	Glu	Thr	Ser	Phe	Gln
		595					600					605			
Ile	Val	Ser	Leu	Asn	Asn	Asp	Gln	Leu	Leu	Lys	Gly	Asp	Phe	Arg	Leu
	610					615					620				
Gln	Pro	Ile	Tyr	Thr	Pro	Asn	Gly	Gly	Ile	Asn	Tyr	Thr	Asp	Cys	His
625					630					635					640
Ile	Pro	Asn	Asn	Met	Arg	Tyr	Cys	Asn	Ser	Ser	Val	Pro	Asp	Leu	Glu
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<210> 29

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 29

cggtctacct gtatggcaac c

<210> 30

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 30
gcaggacaac cagataaacc ac 22

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 31
acgcagattt gagaaggctg tc 22

<210> 32
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 32
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<210> 33
<211> 3449
<212> DNA
<213> Homo sapiens

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<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

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Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile
  1                      5                      10                      15

Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
                20                      25                      30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
  35                      40                      45

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Ser	Ser	Cys	Glu	Asn	Lys	Arg	Ala	Asp	Leu	Val	Phe	Ile	Ile	Asp	Ser	50	55	60
Ser	Arg	Ser	Val	Asn	Thr	His	Asp	Tyr	Ala	Lys	Val	Lys	Glu	Phe	Ile	65	70	75
Val	Asp	Ile	Leu	Gln	Phe	Leu	Asp	Ile	Gly	Pro	Asp	Val	Thr	Arg	Val	85	90	95
Gly	Leu	Leu	Gln	Tyr	Gly	Ser	Thr	Val	Lys	Asn	Glu	Phe	Ser	Leu	Lys	100	105	110
Thr	Phe	Lys	Arg	Lys	Ser	Glu	Val	Glu	Arg	Ala	Val	Lys	Arg	Met	Arg	115	120	125
His	Leu	Ser	Thr	Gly	Thr	Met	Thr	Gly	Leu	Ala	Ile	Gln	Tyr	Ala	Leu	130	135	140
Asn	Ile	Ala	Phe	Ser	Glu	Ala	Glu	Gly	Ala	Arg	Pro	Leu	Arg	Glu	Asn	145	150	155
Val	Pro	Arg	Val	Ile	Met	Ile	Val	Thr	Asp	Gly	Arg	Pro	Gln	Asp	Ser	165	170	175
Val	Ala	Glu	Val	Ala	Ala	Lys	Ala	Arg	Asp	Thr	Gly	Ile	Leu	Ile	Phe	180	185	190
Ala	Ile	Gly	Val	Gly	Gln	Val	Asp	Phe	Asn	Thr	Leu	Lys	Ser	Ile	Gly	195	200	205
Ser	Glu	Pro	His	Glu	Asp	His	Val	Phe	Leu	Val	Ala	Asn	Phe	Ser	Gln	210	215	220
Ile	Glu	Thr	Leu	Thr	Ser	Val	Phe	Gln	Lys	Lys	Leu	Cys	Thr	Ala	His	225	230	235
Met	Cys	Ser	Thr	Leu	Glu	His	Asn	Cys	Ala	His	Phe	Cys	Ile	Asn	Ile	245	250	255
Pro	Gly	Ser	Tyr	Val	Cys	Arg	Cys	Lys	Gln	Gly	Tyr	Ile	Leu	Asn	Ser	260	265	270
Asp	Gln	Thr	Thr	Cys	Arg	Ile	Gln	Asp	Leu	Cys	Ala	Met	Glu	Asp	His	275	280	285
Asn	Cys	Glu	Gln	Leu	Cys	Val	Asn	Val	Pro	Gly	Ser	Phe	Val	Cys	Gln	290	295	300
Cys	Tyr	Ser	Gly	Tyr	Ala	Leu	Ala	Glu	Asp	Gly	Lys	Arg	Cys	Val	Ala	305	310	315
Val	Asp	Tyr	Cys	Ala	Ser	Glu	Asn	His	Gly	Cys	Glu	His	Glu	Cys	Val	325	330	335
Asn	Ala	Asp	Gly	Ser	Tyr	Leu	Cys	Gln	Cys	His	Glu	Gly	Phe	Ala	Leu	340	345	350

Asn	Pro	Asp	Glu	Lys	Thr	Cys	Thr	Arg	Ile	Asn	Tyr	Cys	Ala	Leu	Asn		
		355					360					365					
Lys	Pro	Gly	Cys	Glu	His	Glu	Cys	Val	Asn	Met	Glu	Glu	Ser	Tyr	Tyr		
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Cys	Arg	Cys	His	Arg	Gly	Tyr	Thr	Leu	Asp	Pro	Asn	Gly	Lys	Thr	Cys		
385					390					395					400		
Ser	Arg	Val	Asp	His	Cys	Ala	Gln	Gln	Asp	His	Gly	Cys	Glu	Gln	Leu		
			405						410					415			
Cys	Leu	Asn	Thr	Glu	Asp	Ser	Phe	Val	Cys	Gln	Cys	Ser	Glu	Gly	Phe		
			420					425					430				
Leu	Ile	Asn	Glu	Asp	Leu	Lys	Thr	Cys	Ser	Arg	Val	Asp	Tyr	Cys	Leu		
	435						440					445					
Leu	Ser	Asp	His	Gly	Cys	Glu	Tyr	Ser	Cys	Val	Asn	Met	Asp	Arg	Ser		
450						455					460						
Phe	Ala	Cys	Gln	Cys	Pro	Glu	Gly	His	Val	Leu	Arg	Ser	Asp	Gly	Lys		
465					470					475					480		
Thr	Cys	Ala	Lys	Leu	Asp	Ser	Cys	Ala	Leu	Gly	Asp	His	Gly	Cys	Glu		
			485						490					495			
His	Ser	Cys	Val	Ser	Ser	Glu	Asp	Ser	Phe	Val	Cys	Gln	Cys	Phe	Glu		
			500					505					510				
Gly	Tyr	Ile	Leu	Arg	Glu	Asp	Gly	Lys	Thr	Cys	Arg	Arg	Lys	Asp	Val		
	515						520					525					
Cys	Gln	Ala	Ile	Asp	His	Gly	Cys	Glu	His	Ile	Cys	Val	Asn	Ser	Asp		
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Asp	Ser	Tyr	Thr	Cys	Glu	Cys	Leu	Glu	Gly	Phe	Arg	Leu	Ala	Glu	Asp		
545				550					555						560		
Gly	Lys	Arg	Cys	Arg	Arg	Lys	Asp	Val	Cys	Lys	Ser	Thr	His	His	Gly		
			565					570						575			
Cys	Glu	His	Ile	Cys	Val	Asn	Asn	Gly	Asn	Ser	Tyr	Ile	Cys	Lys	Cys		
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Ser	Glu	Gly	Phe	Val	Leu	Ala	Glu	Asp	Gly	Arg	Arg	Cys	Lys	Lys	Cys		
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Thr	Glu	Gly	Pro	Ile	Asp	Leu	Val	Phe	Val	Ile	Asp	Gly	Ser	Lys	Ser		
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Leu	Gly	Glu	Glu	Asn	Phe	Glu	Val	Val	Lys	Gln	Phe	Val	Thr	Gly	Ile		
625				630						635					640		
Ile	Asp	Ser	Leu	Thr	Ile	Ser	Pro	Lys	Ala	Ala	Arg	Val	Gly	Leu	Leu		
			645						650					655			

Gln	Tyr	Ser	Thr	Gln	Val	His	Thr	Glu	Phe	Thr	Leu	Arg	Asn	Phe	Asn	
			660					665					670			
Ser	Ala	Lys	Asp	Met	Lys	Lys	Ala	Val	Ala	His	Met	Lys	Tyr	Met	Gly	
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705					710					715					720	
Ala	Ala	Ile	Val	Phe	Thr	Asp	Gly	Arg	Ala	Gln	Asp	Asp	Val	Ser	Glu	
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Trp	Ala	Ser	Lys	Ala	Lys	Ala	Asn	Gly	Ile	Thr	Met	Tyr	Ala	Val	Gly	
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Val	Gly	Lys	Ala	Ile	Glu	Glu	Glu	Leu	Gln	Glu	Ile	Ala	Ser	Glu	Pro	
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Thr	Asn	Lys	His	Leu	Phe	Tyr	Ala	Glu	Asp	Phe	Ser	Thr	Met	Asp	Glu	
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Ile	Ser	Glu	Lys	Leu	Lys	Lys	Gly	Ile	Cys	Glu	Ala	Leu	Glu	Asp	Ser	
785					790					795					800	
Asp	Gly	Arg	Gln	Asp	Ser	Pro	Ala	Gly	Glu	Leu	Pro	Lys	Thr	Val	Gln	
				805					810					815		
Gln	Pro	Thr	Glu	Ser	Glu	Pro	Val	Thr	Ile	Asn	Ile	Gln	Asp	Leu	Leu	
			820					825					830			
Ser	Cys	Ser	Asn	Phe	Ala	Val	Gln	His	Arg	Tyr	Leu	Phe	Glu	Glu	Asp	
		835					840					845				
Asn	Leu	Leu	Arg	Ser	Thr	Gln	Lys	Leu	Ser	His	Ser	Thr	Lys	Pro	Ser	
						855					860					
Gly	Ser	Pro	Leu	Glu	Glu	Lys	His	Asp	Gln	Cys	Lys	Cys	Glu	Asn	Leu	
865					870					875					880	
Ile	Met	Phe	Gln	Asn	Leu	Ala	Asn	Glu	Glu	Val	Arg	Lys	Leu	Thr	Gln	
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<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<210> 36
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 36
acagccatgg tctatagctt gg 22

<210> 37
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 37
gcctgtcagt gtcctgaggg acacgtgctc cgcagc gatg ggaag 45

<210> 38
<211> 1813
<212> DNA
<213> Homo sapiens

<400> 38
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gggccatgat ttccctcccg gggcccctgg tgaccaactt gctgcggttt ttgttcctgg 180
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<210> 39
 <211> 390
 <212> PRT
 <213> Homo sapiens

<400> 39

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Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln
      20               25               30

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val
      35               40               45

Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln
      50               55               60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys
      65               70               75               80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro
      85               90               95

Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg
      100              105              110

Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val
      115              120              125

Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr
      130              135              140

Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu
      145              150              155              160

Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser
      165              170              175

Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro
      180              185              190

Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser
      195              200              205

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Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys
 210 215 220
 Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
 225 230 235 240
 Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly
 245 250 255
 Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His
 260 265 270
 Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp
 275 280 285
 Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
 290 295 300
 Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
 305 310 315 320
 Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
 325 330 335
 Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
 340 345 350
 Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
 355 360 365
 Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
 370 375 380
 Gln Ala Gly Ser Leu Val
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 40

agggtctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 41	
attgtgggcc ttgcagacat agac	24
<210> 42	
<211> 50	
<212> DNA	
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 42	
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc	50
<210> 43	
<211> 18	
<212> DNA	
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gtgtgacaca gcgtgggc	18
<210> 44	
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<400> 44	
gaccggcagg cttctgcg	18
<210> 45	
<211> 25	
<212> DNA	
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 45	
cagcagcttc agccaccagg agtgg	25
<210> 46	
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<212> DNA	
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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 46

ctgagccgtg ggctgcagtc tcgc

24

<210> 47

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 47

ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc

45

<210> 48

<211> 2822

<212> DNA

<213> Homo sapiens

<400> 48

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gtgaaatacg	caatggaatt	gaagcctgct	attgcaacat	gggattttca	ggaaatgggtg	180
tcacaatttg	tgaagatgat	aatgaatgtg	gaaatttaac	tcagtcctgt	ggcgaaaatg	240
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<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

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      20              25              30

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
      35              40              45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
      50              55              60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
      65              70              75              80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
      85              90              95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
      100             105             110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
      115             120             125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
      130             135             140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
      145             150             155             160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
      165             170             175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr
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Gln	Lys	Thr	Thr	Glu	Phe	Asp	Thr	Asn	Ser	Thr	Asp	Ile	Ala	Leu	Lys	245	250	255
Val	Phe	Phe	Phe	Asp	Ser	Tyr	Asn	Met	Lys	His	Ile	His	Pro	His	Met	260	265	270
Asn	Met	Asp	Gly	Asp	Tyr	Ile	Asn	Ile	Phe	Pro	Lys	Arg	Lys	Ala	Ala	275	280	285
Tyr	Asp	Ser	Asn	Gly	Asn	Val	Ala	Val	Ala	Phe	Leu	Tyr	Tyr	Lys	Ser	290	295	300
Ile	Gly	Pro	Leu	Leu	Ser	Ser	Ser	Asp	Asn	Phe	Leu	Leu	Lys	Pro	Gln	305	310	315
Asn	Tyr	Asp	Asn	Ser	Glu	Glu	Glu	Glu	Arg	Val	Ile	Ser	Ser	Val	Ile	325	330	335
Ser	Val	Ser	Met	Ser	Ser	Asn	Pro	Pro	Thr	Leu	Tyr	Glu	Leu	Glu	Lys	340	345	350
Ile	Thr	Phe	Thr	Leu	Ser	His	Arg	Lys	Val	Thr	Asp	Arg	Tyr	Arg	Ser	355	360	365
Leu	Cys	Ala	Phe	Trp	Asn	Tyr	Ser	Pro	Asp	Thr	Met	Asn	Gly	Ser	Trp	370	375	380
Ser	Ser	Glu	Gly	Cys	Glu	Leu	Thr	Tyr	Ser	Asn	Glu	Thr	His	Thr	Ser	385	390	395
Cys	Arg	Cys	Asn	His	Leu	Thr	His	Phe	Ala	Ile	Leu	Met	Ser	Ser	Gly	405	410	415
Pro	Ser	Ile	Gly	Ile	Lys	Asp	Tyr	Asn	Ile	Leu	Thr	Arg	Ile	Thr	Gln	420	425	430
Leu	Gly	Ile	Ile	Ile	Ser	Leu	Ile	Cys	Leu	Ala	Ile	Cys	Ile	Phe	Thr	435	440	445
Phe	Trp	Phe	Phe	Ser	Glu	Ile	Gln	Ser	Thr	Arg	Thr	Thr	Ile	His	Lys	450	455	460
Asn	Leu	Cys	Cys	Ser	Leu	Phe	Leu	Ala	Glu	Leu	Val	Phe	Leu	Val	Gly	465	470	475
Ile	Asn	Thr	Asn	Thr	Asn	Lys	Leu	Phe	Cys	Ser	Ile	Ile	Ala	Gly	Leu	485	490	495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
675 680 685

Leu Arg
690

<210> 50

<211> 589

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (61)..(61)

<223> a, t, c or g

<400> 50

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gtattggtcc ctttgctttc atcatctgac aacttcttat tgaaacctca aaattatgat 180
aattctgaag aggaggaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
ccaccacat tatatgaact tgaaaaaata acatttacat taagtcacg aaaggtcaca 300
gataggtata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360

tgggtcttcag agggctgtga gctgacatac tcaaatagaga cccacacctc atgccgctgt 420
 aatcacctga cacattttgc aattttgatg tcctctgggc cttccattgg tattaaagat 480
 tataatatcc ttacaaggat cactcaacta ggaataatta tttcactgat ttgtcttgcc 540
 atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

<210> 51
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 51
 ggtaatgagc tccattacag 20

<210> 52
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 52
 ggagtagaaa gcgcatgg 18

<210> 53
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 53
 cacctgatac catgaatggc ag 22

<210> 54
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 54
 cgagctcgaa ttaattcg 18

<210> 55
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 55

ggatctcctg agctcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 57

atgagacca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

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gggacaagaa gccgccgcct gcctgcccgg gcccggggag ggggctgggg ctggggcccg 180
aggcgggggtg tgagtgggtg tgtgcggggg gcggaggctt gatgcaatcc cgataagaaa 240
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acccccatcg ccggagctgc gccgagagcc ccaggagggt gccatgcgga gcgggtgtgt 480
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ggaggccgtg aggagtccca gctttgagaa gtaactgaga ccatgcccgg gcctcttcac 1140


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```

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

```

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
          20              25              30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
      35              40              45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
      50              55              60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
      65              70              75              80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
          85              90              95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
      100              105              110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
      115              120              125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
      130              135              140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
      145              150              155              160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
          165              170              175

```

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
195 200 205

Val Arg Ser Pro Ser Phe Glu Lys
210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 60

atccgcccag atggctacaa tgtgta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 61

gcctcccgggt ctccctgagc agtgccaaac agcggcagtg ta

42

<210> 62

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 62

ccagtccgggt gacaagccca aa

22

<210> 63

<211> 1295

<212> DNA

<213> Homo sapiens

<400> 63

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ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360

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<210> 64

<211> 312

<212> PRT

<213> Homo sapiens

<400> 64

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Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Leu Arg Tyr
  1              5              10              15

```

```

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
      20              25              30

```

```

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
      35              40              45

```

```

Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
      50              55              60

```

```

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
      65              70              75              80

```

```

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
      85              90              95

```

```

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
      100             105             110

```

```

Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
      115             120             125

```

```

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
      130             135             140

```

```

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
      145             150             155             160

```

```

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
      165             170             175

```

```

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met

```

180										185					190				
Asn	Thr	Lys	Thr	Gly	Thr	Leu	Gln	Phe	Asn	Thr	Val	Ser	Lys	Leu	Asp				
		195					200					205							
Thr	Gly	Glu	Tyr	Ser	Cys	Glu	Ala	Arg	Asn	Ser	Val	Gly	Tyr	Arg	Arg				
	210					215					220								
Cys	Pro	Gly	Lys	Arg	Met	Gln	Val	Asp	Asp	Leu	Asn	Ile	Ser	Gly	Ile				
225					230					235					240				
Ile	Ala	Ala	Val	Val	Val	Val	Ala	Leu	Val	Ile	Ser	Val	Cys	Gly	Leu				
			245						250					255					
Gly	Val	Cys	Tyr	Ala	Gln	Arg	Lys	Gly	Tyr	Phe	Ser	Lys	Glu	Thr	Ser				
			260					265					270						
Phe	Gln	Lys	Ser	Asn	Ser	Ser	Ser	Lys	Ala	Thr	Thr	Met	Ser	Glu	Asn				
		275					280					285							
Val	Gln	Trp	Leu	Thr	Pro	Val	Ile	Pro	Ala	Leu	Trp	Lys	Ala	Ala	Ala				
	290					295					300								
Gly	Gly	Ser	Arg	Gly	Gln	Glu	Phe												
305					310														

<210> 65

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 65

atcgttgatga agttagtgcc cc

22

<210> 66

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 66

acctgcgata tccaacagaa ttg

23

<210> 67

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 67

ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc

48

<210> 68

<211> 2639

<212> DNA

<213> Homo sapiens

<400> 68

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gcatcatgct	gctattcctg	caaatactga	agaagcatgg	gatttaaata	ttttacttct	180
aaataaatga	attactcaat	ctcctatgac	catctataca	tactccacct	tcaaaaagta	240
catcaatatt	atatcattaa	ggaaatagta	accttctctt	ctccaatatg	catgacattt	300
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<210> 69

<211> 708
<212> PRT
<213> Homo sapiens

<400> 69

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			20					25					30			
Cys	Thr	Cys	Glu	Ile	Arg	Pro	Trp	Phe	Thr	Pro	Arg	Ser	Ile	Tyr	Met	
		35					40					45				
Glu	Ala	Ser	Thr	Val	Asp	Cys	Asn	Asp	Leu	Gly	Leu	Leu	Thr	Phe	Pro	
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Ala	Arg	Leu	Pro	Ala	Asn	Thr	Gln	Ile	Leu	Leu	Leu	Gln	Thr	Asn	Asn	
65					70					75					80	
Ile	Ala	Lys	Ile	Glu	Tyr	Ser	Thr	Asp	Phe	Pro	Val	Asn	Leu	Thr	Gly	
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Leu	Asp	Leu	Ser	Gln	Asn	Asn	Leu	Ser	Ser	Val	Thr	Asn	Ile	Asn	Val	
			100					105					110			
Lys	Lys	Met	Pro	Gln	Leu	Leu	Ser	Val	Tyr	Leu	Glu	Glu	Asn	Lys	Leu	
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Thr	Glu	Leu	Pro	Glu	Lys	Cys	Leu	Ser	Glu	Leu	Ser	Asn	Leu	Gln	Glu	
	130					135						140				
Leu	Tyr	Ile	Asn	His	Asn	Leu	Leu	Ser	Thr	Ile	Ser	Pro	Gly	Ala	Phe	
145					150					155					160	
Ile	Gly	Leu	His	Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Arg	Leu	
				165					170					175		
Gln	Met	Ile	Asn	Ser	Lys	Trp	Phe	Asp	Ala	Leu	Pro	Asn	Leu	Glu	Ile	
			180					185					190			
Leu	Met	Ile	Gly	Glu	Asn	Pro	Ile	Ile	Arg	Ile	Lys	Asp	Met	Asn	Phe	
		195					200					205				
Lys	Pro	Leu	Ile	Asn	Leu	Arg	Ser	Leu	Val	Ile	Ala	Gly	Ile	Asn	Leu	
	210					215					220					
Thr	Glu	Ile	Pro	Asp	Asn	Ala	Leu	Val	Gly	Leu	Glu	Asn	Leu	Glu	Ser	
225					230					235					240	
Ile	Ser	Phe	Tyr	Asp	Asn	Arg	Leu	Ile	Lys	Val	Pro	His	Val	Ala	Leu	
				245					250					255		
Gln	Lys	Val	Val	Asn	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	Asn	Pro	Ile	
			260					265					270			
Asn	Arg	Ile	Arg	Arg	Gly	Asp	Phe	Ser	Asn	Met	Leu	His	Leu	Lys	Glu	

275					280					285					
Leu	Gly	Ile	Asn	Asn	Met	Pro	Glu	Leu	Ile	Ser	Ile	Asp	Ser	Leu	Ala
290						295					300				
Val	Asp	Asn	Leu	Pro	Asp	Leu	Arg	Lys	Ile	Glu	Ala	Thr	Asn	Asn	Pro
305					310					315					320
Arg	Leu	Ser	Tyr	Ile	His	Pro	Asn	Ala	Phe	Phe	Arg	Leu	Pro	Lys	Leu
				325					330					335	
Glu	Ser	Leu	Met	Leu	Asn	Ser	Asn	Ala	Leu	Ser	Ala	Leu	Tyr	His	Gly
			340					345					350		
Thr	Ile	Glu	Ser	Leu	Pro	Asn	Leu	Lys	Glu	Ile	Ser	Ile	His	Ser	Asn
		355					360					365			
Pro	Ile	Arg	Cys	Asp	Cys	Val	Ile	Arg	Trp	Met	Asn	Met	Asn	Lys	Thr
	370					375					380				
Asn	Ile	Arg	Phe	Met	Glu	Pro	Asp	Ser	Leu	Phe	Cys	Val	Asp	Pro	Pro
385					390					395					400
Glu	Phe	Gln	Gly	Gln	Asn	Val	Arg	Gln	Val	His	Phe	Arg	Asp	Met	Met
				405					410					415	
Glu	Ile	Cys	Leu	Pro	Leu	Ile	Ala	Pro	Glu	Ser	Phe	Pro	Ser	Asn	Leu
			420					425					430		
Asn	Val	Glu	Ala	Gly	Ser	Tyr	Val	Ser	Phe	His	Cys	Arg	Ala	Thr	Ala
		435					440					445			
Glu	Pro	Gln	Pro	Glu	Ile	Tyr	Trp	Ile	Thr	Pro	Ser	Gly	Gln	Lys	Leu
	450					455					460				
Leu	Pro	Asn	Thr	Leu	Thr	Asp	Lys	Phe	Tyr	Val	His	Ser	Glu	Gly	Thr
465					470					475					480
Leu	Asp	Ile	Asn	Gly	Val	Thr	Pro	Lys	Glu	Gly	Gly	Leu	Tyr	Thr	Cys
				485					490					495	
Ile	Ala	Thr	Asn	Leu	Val	Gly	Ala	Asp	Leu	Lys	Ser	Val	Met	Ile	Lys
			500					505					510		
Val	Asp	Gly	Ser	Phe	Pro	Gln	Asp	Asn	Asn	Gly	Ser	Leu	Asn	Ile	Lys
	515						520					525			
Ile	Arg	Asp	Ile	Gln	Ala	Asn	Ser	Val	Leu	Val	Ser	Trp	Lys	Ala	Ser
	530					535					540				
Ser	Lys	Ile	Leu	Lys	Ser	Ser	Val	Lys	Trp	Thr	Ala	Phe	Val	Lys	Thr
545					550					555					560
Glu	Asn	Ser	His	Ala	Ala	Gln	Ser	Ala	Arg	Ile	Pro	Ser	Asp	Val	Lys
				565					570					575	
Val	Tyr	Asn	Leu	Thr	His	Leu	Asn	Pro	Ser	Thr	Glu	Tyr	Lys	Ile	Cys

580	585	590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620
Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile		
625	630	635
Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp		
645	650	655
Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala		
660	665	670
Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys		
675	680	685
Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro		
690	695	700
Thr Asn Met Ser		
705		

<210> 70
 <211> 1305
 <212> DNA
 <213> Homo sapiens

<400> 70

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agctgcagcc	ttttgaaaca	cgcaagaagg	aatcaatag	tgtggacagg	gctggaacct	120
ttaccacgct	tgttggagta	gatgaggaat	gggctcgtga	ttatgctgac	attccagcat	180
gaatctggta	gacctgtggt	taacccggtc	cctctccatg	tgtctcctcc	tacaaagttt	240
tggtcttatg	atactgtgct	ttcattctgc	cagtatgtgt	ccaagggtc	gtctttgttc	300
ttcctctggg	ggtttaaatg	tcacctgtag	caatgcaaat	ctcaaggaaa	tacctagaga	360
tcttcctcct	gaaacagtct	tactgtatct	ggactccaat	cagatcacat	ctattcccaa	420
tgaatttttt	aaggacctcc	atcaactgag	agttctcaac	ctgtccaaaa	atggcattga	480
gtttatcgat	gagcatgcct	tcaaaggagt	agctgaaacc	ttgcagactc	tggacttgtc	540
cgacaatcgg	attcaaagtg	tgcacaaaaa	tgctttcaat	aacctgaagg	ccagggccag	600
aattgccaac	aacctctggc	actgcgactg	tactctacag	caagttctga	ggagcatggc	660
gtccaatcat	gagacagccc	acaacgtgat	ctgtaaaacg	tccgtgttgg	atgaacatgc	720
tggcagacca	ttcctcaatg	ctgccaacga	cgctgacctt	tgtaacctcc	ctaaaaaac	780
taccgattat	gccatgctgg	tcaccatggt	tggctgggtc	actatggtga	tctcatatgt	840
ggtatattat	gtgaggcaaa	atcaggagga	tgcccggaga	cacctcgaat	acttgaaatc	900
cctgccaaagc	aggcagaaga	aagcagatga	acctgatgat	attagcactg	tggtatagt	960
tccaaactga	ctgtcattga	gaaagaaaga	aagtagtttg	cgattgcagt	agaaataagt	1020
ggtttacttc	tcccatccat	tgtaaacatt	tgaaactttg	tatttcagtt	ttttttgaat	1080
tatgccactg	ctgaactttt	aacaaacact	acaacataaa	taatttgagt	ttaggtgatc	1140
caccctttaa	ttgtaccccc	gatggtatat	ttctgagtaa	gctactatct	gaacattagt	1200
tagatccatc	tcactattta	ataatgaaat	ttattttttt	aattttaaag	caaataaaa	1260
cttaactttg	aaccatggga	aaaaaaaaaa	aaaaaaaaaa	aaaca		1305

<210> 71
 <211> 259

<212> PRT

<213> Homo sapiens

<400> 71

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Leu	Leu	Gln	Ser	Phe	Val	Leu	Met	Ile	Leu	Cys	Phe	His	Ser	Ala	Ser	
			20					25					30			
Met	Cys	Pro	Lys	Gly	Cys	Leu	Cys	Ser	Ser	Ser	Gly	Gly	Leu	Asn	Val	
		35					40					45				
Thr	Cys	Ser	Asn	Ala	Asn	Leu	Lys	Glu	Ile	Pro	Arg	Asp	Leu	Pro	Pro	
	50					55					60					
Glu	Thr	Val	Leu	Leu	Tyr	Leu	Asp	Ser	Asn	Gln	Ile	Thr	Ser	Ile	Pro	
65					70					75					80	
Asn	Glu	Ile	Phe	Lys	Asp	Leu	His	Gln	Leu	Arg	Val	Leu	Asn	Leu	Ser	
				85					90					95		
Lys	Asn	Gly	Ile	Glu	Phe	Ile	Asp	Glu	His	Ala	Phe	Lys	Gly	Val	Ala	
			100					105					110			
Glu	Thr	Leu	Gln	Thr	Leu	Asp	Leu	Ser	Asp	Asn	Arg	Ile	Gln	Ser	Val	
		115					120					125				
His	Lys	Asn	Ala	Phe	Asn	Asn	Leu	Lys	Ala	Arg	Ala	Arg	Ile	Ala	Asn	
	130					135					140					
Asn	Pro	Trp	His	Cys	Asp	Cys	Thr	Leu	Gln	Gln	Val	Leu	Arg	Ser	Met	
145					150					155					160	
Ala	Ser	Asn	His	Glu	Thr	Ala	His	Asn	Val	Ile	Cys	Lys	Thr	Ser	Val	
				165					170					175		
Leu	Asp	Glu	His	Ala	Gly	Arg	Pro	Phe	Leu	Asn	Ala	Ala	Asn	Asp	Ala	
			180					185						190		
Asp	Leu	Cys	Asn	Leu	Pro	Lys	Lys	Thr	Thr	Asp	Tyr	Ala	Met	Leu	Val	
		195					200					205				
Thr	Met	Phe	Gly	Trp	Phe	Thr	Met	Val	Ile	Ser	Tyr	Val	Val	Tyr	Tyr	
	210					215					220					
Val	Arg	Gln	Asn	Gln	Glu	Asp	Ala	Arg	Arg	His	Leu	Glu	Tyr	Leu	Lys	
225					230					235					240	
Ser	Leu	Pro	Ser	Arg	Gln	Lys	Lys	Ala	Asp	Glu	Pro	Asp	Asp	Ile	Ser	
				245					250					255		
Thr	Val	Val														

<210> 72

<211> 2290

<212> DNA
<213> Homo sapiens

<400> 72

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tgctgggctc agtgctgtca ggctcggccca cgggctgccc gccccgctgc gagtgtctccg 180
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agttcgccag cttcccgcac ctggaggagc tggagctcaa cgagaacatc gtgagcgccg 360
tggagcccgg cgccttcaac aacctcttca acctccggac gctgggtctc cgcagcaacc 420
gcctgaagct catcccgcta ggcgctcttca ctggcctcag caacctgacc aagcaggaca 480
tcagcgagaa caagatcggt atcctactgg actacatggt tcaggacctg tacaacctca 540
agtcactgga ggttggcgac aatgacctcg tctacatctc tcaccgcgcc ttcagcggcc 600
tcaacagcct ggagcagctg acgctggaga aatgcaacct gacctccatc cccaccgagg 660
cgctgtccca cctgcacggc ctcatcgctc tgaggctccg gcacctcaac atcaatgcca 720
tccgggacta ctccttcaag aggctgtacc gactcaaggt cttggagatc tcccactggc 780
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tcacacactg caatctgacc gctgtgcctt acctggcgtt ccgccaccta gtctatctcc 900
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ggcagagtca ataattcaat aaaaaagtta cgaactttct ctgtaacttg ggtttcaata 2220
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<210> 73
<211> 620
<212> PRT
<213> Homo sapiens

<400> 73

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Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly
                20                      25                      30
Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
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35					40					45					
Ser	Ala	Gln	Asp	Arg	Ala	Val	Leu	Cys	His	Arg	Lys	Cys	Phe	Val	Ala
50					55					60					
Val	Pro	Glu	Gly	Ile	Pro	Thr	Glu	Thr	Arg	Leu	Leu	Asp	Leu	Gly	Lys
65					70					75					80
Asn	Arg	Ile	Lys	Thr	Leu	Asn	Gln	Asp	Glu	Phe	Ala	Ser	Phe	Pro	His
			85						90					95	
Leu	Glu	Glu	Leu	Glu	Leu	Asn	Glu	Asn	Ile	Val	Ser	Ala	Val	Glu	Pro
			100					105					110		
Gly	Ala	Phe	Asn	Asn	Leu	Phe	Asn	Leu	Arg	Thr	Leu	Gly	Leu	Arg	Ser
		115					120					125			
Asn	Arg	Leu	Lys	Leu	Ile	Pro	Leu	Gly	Val	Phe	Thr	Gly	Leu	Ser	Asn
						135					140				
Leu	Thr	Lys	Gln	Asp	Ile	Ser	Glu	Asn	Lys	Ile	Val	Ile	Leu	Leu	Asp
145					150					155					160
Tyr	Met	Phe	Gln	Asp	Leu	Tyr	Asn	Leu	Lys	Ser	Leu	Glu	Val	Gly	Asp
				165					170					175	
Asn	Asp	Leu	Val	Tyr	Ile	Ser	His	Arg	Ala	Phe	Ser	Gly	Leu	Asn	Ser
			180					185					190		
Leu	Glu	Gln	Leu	Thr	Leu	Glu	Lys	Cys	Asn	Leu	Thr	Ser	Ile	Pro	Thr
			195				200					205			
Glu	Ala	Leu	Ser	His	Leu	His	Gly	Leu	Ile	Val	Leu	Arg	Leu	Arg	His
						215					220				
Leu	Asn	Ile	Asn	Ala	Ile	Arg	Asp	Tyr	Ser	Phe	Lys	Arg	Leu	Tyr	Arg
225					230					235					240
Leu	Lys	Val	Leu	Glu	Ile	Ser	His	Trp	Pro	Tyr	Leu	Asp	Thr	Met	Thr
				245					250					255	
Pro	Asn	Cys	Leu	Tyr	Gly	Leu	Asn	Leu	Thr	Ser	Leu	Ser	Ile	Thr	His
			260					265					270		
Cys	Asn	Leu	Thr	Ala	Val	Pro	Tyr	Leu	Ala	Val	Arg	His	Leu	Val	Tyr
			275				280					285			
Leu	Arg	Phe	Leu	Asn	Leu	Ser	Tyr	Asn	Pro	Ile	Ser	Thr	Ile	Glu	Gly
				295							300				
Ser	Met	Leu	His	Glu	Leu	Leu	Arg	Leu	Gln	Glu	Ile	Gln	Leu	Val	Gly
305					310					315					320
Gly	Gln	Leu	Ala	Val	Val	Glu	Pro	Tyr	Ala	Phe	Arg	Gly	Leu	Asn	Tyr
				325					330					335	
Leu	Arg	Val	Leu	Asn	Val	Ser	Gly	Asn	Gln	Leu	Thr	Thr	Leu	Glu	Glu

340					345					350						
Ser	Val	Phe	His	Ser	Val	Gly	Asn	Leu	Glu	Thr	Leu	Ile	Leu	Asp	Ser	
355					360					365						
Asn	Pro	Leu	Ala	Cys	Asp	Cys	Arg	Leu	Leu	Trp	Val	Phe	Arg	Arg	Arg	
370					375					380						
Trp	Arg	Leu	Asn	Phe	Asn	Arg	Gln	Gln	Pro	Thr	Cys	Ala	Thr	Pro	Glu	
385					390					395					400	
Phe	Val	Gln	Gly	Lys	Glu	Phe	Lys	Asp	Phe	Pro	Asp	Val	Leu	Leu	Pro	
405					410					415						
Asn	Tyr	Phe	Thr	Cys	Arg	Arg	Ala	Arg	Ile	Arg	Asp	Arg	Lys	Ala	Gln	
420					425					430						
Gln	Val	Phe	Val	Asp	Glu	Gly	His	Thr	Val	Gln	Phe	Val	Cys	Arg	Ala	
435					440					445						
Asp	Gly	Asp	Pro	Pro	Pro	Ala	Ile	Leu	Trp	Leu	Ser	Pro	Arg	Lys	His	
450					455					460						
Leu	Val	Ser	Ala	Lys	Ser	Asn	Gly	Arg	Leu	Thr	Val	Phe	Pro	Asp	Gly	
465					470					475					480	
Thr	Leu	Glu	Val	Arg	Tyr	Ala	Gln	Val	Gln	Asp	Asn	Gly	Thr	Tyr	Leu	
485					490					495						
Cys	Ile	Ala	Ala	Asn	Ala	Gly	Gly	Asn	Asp	Ser	Met	Pro	Ala	His	Leu	
500					505					510						
His	Val	Arg	Ser	Tyr	Ser	Pro	Asp	Trp	Pro	His	Gln	Pro	Asn	Lys	Thr	
515					520					525						
Phe	Ala	Phe	Ile	Ser	Asn	Gln	Pro	Gly	Glu	Gly	Glu	Ala	Asn	Ser	Thr	
530					535					540						
Arg	Ala	Thr	Val	Pro	Phe	Pro	Phe	Asp	Ile	Lys	Thr	Leu	Ile	Ile	Ala	
545					550					555					560	
Thr	Thr	Met	Gly	Phe	Ile	Ser	Phe	Leu	Gly	Val	Val	Leu	Phe	Cys	Leu	
565					570					575						
Val	Leu	Leu	Phe	Leu	Trp	Ser	Arg	Gly	Lys	Gly	Asn	Thr	Lys	His	Asn	
580					585					590						
Ile	Glu	Ile	Glu	Tyr	Val	Pro	Arg	Lys	Ser	Asp	Ala	Gly	Ile	Ser	Ser	
595					600					605						
Ala	Asp	Ala	Pro	Arg	Lys	Phe	Asn	Met	Lys	Met	Ile					
610					615					620						

<210> 74

<211> 22

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 74
 tcacctggag cctttattgg cc 22

<210> 75
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 75
 ataccagcta taaccaggct gcg 23

<210> 76
 <211> 52
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 76
 caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg 50
 gg 52

<210> 77
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 77
 ccatgtgtct cctcctacaa ag 22

<210> 78
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 78
 gggaatagat gtgatctgat tgg 23

<210> 79
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 79
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 <210> 80
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 80
 agcaaccgcc tgaagctcat cc 22

 <210> 81
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 81
 aaggcgcggt gaaagatgta gacg 24

 <210> 82
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 82
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 <210> 83
 <211> 1685
 <212> DNA
 <213> Homo sapiens

 <400> 83
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 agccagggag ccggccggga agcgcgatgg gggccccagc cgctcgtc ctgctcctgc 180

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tcctgctgtt cgctgctgc tgggcgcccg gcggggccaa cctctcccag gacgacagcc 240
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tgaaagatca cgaggactca tccctgcaat ggtctaacc tgctcagcag actctctact 360
ttggggagaa gagagccctt cgagataatc gaattcagct ggttacctct acgccccacg 420
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tcttcactat gcctgtgcga actgccaagt ccctcgtcac tgtgctagga attccacaga 540
agcccatcat cactgggttat aaatcttcat tacgggaaaa agacacagcc accctaaact 600
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<210> 84

<211> 398

<212> PRT

<213> Homo sapiens

<400> 84

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      20                      25                      30

Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
  35                      40                      45

Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
  50                      55                      60

Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
  65                      70                      75                      80

Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
      85                      90                      95

Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
  100                      105                      110

Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
  115                      120                      125

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Ile	Pro	Gln	Lys	Pro	Ile	Ile	Thr	Gly	Tyr	Lys	Ser	Ser	Leu	Arg	Glu	130	135	140
Lys	Asp	Thr	Ala	Thr	Leu	Asn	Cys	Gln	Ser	Ser	Gly	Ser	Lys	Pro	Ala	145	150	155
Ala	Arg	Leu	Thr	Trp	Arg	Lys	Gly	Asp	Gln	Glu	Leu	His	Gly	Glu	Pro	165	170	175
Thr	Arg	Ile	Gln	Glu	Asp	Pro	Asn	Gly	Lys	Thr	Phe	Thr	Val	Ser	Ser	180	185	190
Ser	Val	Thr	Phe	Gln	Val	Thr	Arg	Glu	Asp	Asp	Gly	Ala	Ser	Ile	Val	195	200	205
Cys	Ser	Val	Asn	His	Glu	Ser	Leu	Lys	Gly	Ala	Asp	Arg	Ser	Thr	Ser	210	215	220
Gln	Arg	Ile	Glu	Val	Leu	Tyr	Thr	Pro	Thr	Ala	Met	Ile	Arg	Pro	Asp	225	230	235
Pro	Pro	His	Pro	Arg	Glu	Gly	Gln	Lys	Leu	Leu	Leu	His	Cys	Glu	Gly	245	250	255
Arg	Gly	Asn	Pro	Val	Pro	Gln	Gln	Tyr	Leu	Trp	Glu	Lys	Glu	Gly	Ser	260	265	270
Val	Pro	Pro	Leu	Lys	Met	Thr	Gln	Glu	Ser	Ala	Leu	Ile	Phe	Pro	Phe	275	280	285
Leu	Asn	Lys	Ser	Asp	Ser	Gly	Thr	Tyr	Gly	Cys	Thr	Ala	Thr	Ser	Asn	290	295	300
Met	Gly	Ser	Tyr	Lys	Ala	Tyr	Tyr	Thr	Leu	Asn	Val	Asn	Asp	Pro	Ser	305	310	315
Pro	Val	Pro	Ser	Ser	Ser	Ser	Thr	Tyr	His	Ala	Ile	Ile	Gly	Gly	Ile	325	330	335
Val	Ala	Phe	Ile	Val	Phe	Leu	Leu	Leu	Ile	Met	Leu	Ile	Phe	Leu	Gly	340	345	350
His	Tyr	Leu	Ile	Arg	His	Lys	Gly	Thr	Tyr	Leu	Thr	His	Glu	Ala	Lys	355	360	365
Gly	Ser	Asp	Asp	Ala	Pro	Asp	Ala	Asp	Thr	Ala	Ile	Ile	Asn	Ala	Glu	370	375	380
Gly	Gly	Gln	Ser	Gly	Gly	Asp	Asp	Lys	Lys	Glu	Tyr	Phe	Ile			385	390	395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 87

cctagcacag tgacgagga cttggc

26

<210> 88

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 88

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50

<210> 89

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 89

gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt

50

<210> 90

<211> 2755

<212> DNA

<213> Homo sapiens

<400> 90

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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

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Glu Ile Glu Gly	Asp Leu His Val	Asp Cys Glu Lys	Lys Gly Phe Thr
35	40	45	
Ser Leu Gln Arg	Phe Thr Ala Pro	Thr Ser Gln Phe	Tyr His Leu Phe
50	55	60	
Leu His Gly Asn	Ser Leu Thr Arg	Leu Phe Pro Asn	Glu Phe Ala Asn
65	70	75	80
Phe Tyr Asn Ala	Val Ser Leu His	Met Glu Asn Asn	Gly Leu His Glu
85	90	95	
Ile Val Pro Gly	Ala Phe Leu Gly	Leu Gln Leu Val	Lys Arg Leu His
100	105	110	
Ile Asn Asn Asn	Lys Ile Lys Ser	Phe Arg Lys Gln	Thr Phe Leu Gly
115	120	125	
Leu Asp Asp Leu	Glu Tyr Leu Gln	Ala Asp Phe Asn	Leu Leu Arg Asp
130	135	140	
Ile Asp Pro Gly	Ala Phe Gln Asp	Leu Asn Lys Leu	Glu Val Leu Ile
145	150	155	160
Leu Asn Asp Asn	Leu Ile Ser Thr	Leu Pro Ala Asn	Val Phe Gln Tyr
165	170	175	
Val Pro Ile Thr	His Leu Asp Leu	Arg Gly Asn Arg	Leu Lys Thr Leu
180	185	190	
Pro Tyr Glu Glu	Val Leu Glu Gln	Ile Pro Gly Ile	Ala Glu Ile Leu
195	200	205	
Leu Glu Asp Asn	Pro Trp Asp Cys	Thr Cys Asp Leu	Leu Ser Leu Lys
210	215	220	
Glu Trp Leu Glu	Asn Ile Pro Lys	Asn Ala Leu Ile	Gly Arg Val Val
225	230	235	240
Cys Glu Ala Pro	Thr Arg Leu Gln	Gly Lys Asp Leu	Asn Glu Thr Thr
245	250	255	
Glu Gln Asp Leu	Cys Pro Leu Lys	Asn Arg Val Asp	Ser Ser Leu Pro
260	265	270	
Ala Pro Pro Ala	Gln Glu Glu Thr	Phe Ala Pro Gly	Pro Leu Pro Thr
275	280	285	
Pro Phe Lys Thr	Asn Gly Gln Glu	Asp His Ala Thr	Pro Gly Ser Ala
290	295	300	
Pro Asn Gly Gly	Thr Lys Ile Pro	Gly Asn Trp Gln	Ile Lys Ile Arg

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Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala						
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Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly						
	340			345		350
Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala						
	355			360		365
Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp						
	370			375		380
Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn						
	385			390		395
Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn						
	405			410		415
Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser						
	420			425		430
Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn						
	435			440		445
Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro						
	450			455		460
Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn						
	465			470		475
Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu						
	485			490		495
Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala						
	500			505		510
Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly						
	515			520		525
Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala						
	530			535		540
Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr						
	545			550		555
Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu						
	565			570		575
Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His						
	580			585		590
Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser						
	595			600		605
Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu						

610	615	620
Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val		
625	630	635 640
Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser		
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Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr		
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Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp		
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Cys Gly Ser His Ser Leu Ser Asp		
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<210> 92
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 92
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<210> 93
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 93
 attgttgatgc aggctgagtt taag 24

<210> 94
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 94
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<210> 95
 <211> 2226
 <212> DNA
 <213> Homo sapiens

<400> 95

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<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

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Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
  35                      40                      45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
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Pro	Gly	Pro	Gly	Gly	Gly	Ser	Lys	Asp	Leu	Leu	Phe	Trp	Val	Ala	Leu
				85					90					95	
Glu	Arg	Arg	Arg	Ser	His	Cys	Thr	Leu	Glu	Asn	Glu	Pro	Leu	Arg	Gly
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Phe	Ser	Trp	Leu	Ser	Ser	Asp	Pro	Gly	Gly	Leu	Glu	Ser	Asp	Thr	Leu
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Cys	Ala	Thr	Gly	Phe	Glu	Leu	Gly	Lys	Asp	Gly	Arg	Ser	Cys	Val	Thr
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Ile	Arg	Val	Asp	Glu	Lys	Leu	Gly	Glu	Thr	Pro	Leu	Val	Pro	Glu	Gln
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370					375					380						
Ser	Ser	Ala	Thr	Pro	Gln	Ala	Phe	Asp	Ser	Ser	Ser	Ala	Val	Val	Phe	
385					390					395					400	
Ile	Phe	Val	Ser	Thr	Ala	Val	Val	Val	Leu	Val	Ile	Leu	Thr	Met	Thr	
					405					410					415	
Val	Leu	Gly	Leu	Val	Lys	Leu	Cys	Phe	His	Glu	Ser	Pro	Ser	Ser	Gln	
					420					425					430	
Pro	Arg	Lys	Glu	Ser	Met	Gly	Pro	Pro	Gly	Leu	Glu	Ser	Asp	Pro	Glu	
					435					440					445	
Pro	Ala	Ala	Leu	Gly	Ser	Ser	Ser	Ala	His	Cys	Thr	Asn	Asn	Gly	Val	
					450					455					460	
Lys	Val	Gly	Asp	Cys	Asp	Leu	Arg	Asp	Arg	Ala	Glu	Gly	Ala	Leu	Leu	
465					470					475					480	
Ala	Glu	Ser	Pro	Leu	Gly	Ser	Ser	Asp	Ala							
					485					490						

<210> 97

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 97

tggaaggaga tgcgatgcca cctg

24

<210> 98

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 98

tgaccagtgg ggaaggacag

20

<210> 99

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 99

acagagcaga ggggtgccttg

20

<210> 100

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 100

tcagggacaa gtggtgtctc tccc

24

<210> 101

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 101

tcagggaagg agtgtgcagt tctg

24

<210> 102

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 102

acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgctcgct

50

<210> 103

<211> 2026

<212> DNA

<213> Homo sapiens

<400> 103

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tatcccccg ctacctgggc cgccccgcgg cgggtgcgcg gtgagagga ggcgcgggc 180
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gctgccatga ggggcgcgaa cgcctgggcg ccactctgcc tgctgtggc tgccgccacc 360
cagctctcgc ggcagcagtc ccagagaga cctgttttca catgtggtgg cattcttact 420
ggagagtctg gatattattg cagtgaaggt tttcctggag tgtaccctcc aaatagcaaa 480
tgtacttgga aaatcacagt tcccgaagga aaagtagtcg ttctcaattt ccgattcata 540
gacctcgaga gtgacaacct gtgccgctat gactttgtgg atgtgtacaa tggccatgcc 600

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gtgttatttg ttccaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

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<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

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Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
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Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
      20              25              30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
      35              40              45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
      50              55              60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
      65              70              75              80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
      85              90              95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
      100             105             110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
      115             120             125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
      130             135             140

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Glu	Pro	Asn	Glu	Arg	Gly	Asp	Gln	Tyr	Cys	Gly	Gly	Leu	Leu	Asp	Arg	
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				165					170					175		
Ala	Gly	Val	Thr	Cys	Val	Trp	His	Ile	Val	Ala	Pro	Lys	Asn	Gln	Leu	
			180					185					190			
Ile	Glu	Leu	Lys	Phe	Glu	Lys	Phe	Asp	Val	Glu	Arg	Asp	Asn	Tyr	Cys	
		195					200					205				
Arg	Tyr	Asp	Tyr	Val	Ala	Val	Phe	Asn	Gly	Gly	Glu	Val	Asn	Asp	Ala	
	210					215					220					
Arg	Arg	Ile	Gly	Lys	Tyr	Cys	Gly	Asp	Ser	Pro	Pro	Ala	Pro	Ile	Val	
225					230					235					240	
Ser	Glu	Arg	Asn	Glu	Leu	Leu	Ile	Gln	Phe	Leu	Ser	Asp	Leu	Ser	Leu	
			245						250					255		
Thr	Ala	Asp	Gly	Phe	Ile	Gly	His	Tyr	Ile	Phe	Arg	Pro	Lys	Lys	Leu	
		260						265					270			
Pro	Thr	Thr	Thr	Glu	Gln	Pro	Val	Thr	Thr	Thr	Phe	Pro	Val	Thr	Thr	
		275					280					285				
Gly	Leu	Lys	Pro	Thr	Val	Ala	Leu	Cys	Gln	Gln	Lys	Cys	Arg	Arg	Thr	
	290					295					300					
Gly	Thr	Leu	Glu	Gly	Asn	Tyr	Cys	Ser	Ser	Asp	Phe	Val	Leu	Ala	Gly	
305					310					315					320	
Thr	Val	Ile	Thr	Thr	Ile	Thr	Arg	Asp	Gly	Ser	Leu	His	Ala	Thr	Val	
			325						330					335		
Ser	Ile	Ile	Asn	Ile	Tyr	Lys	Glu	Gly	Asn	Leu	Ala	Ile	Gln	Gln	Ala	
			340					345					350			
Gly	Lys	Asn	Met	Ser	Ala	Arg	Leu	Thr	Val	Val	Cys	Lys	Gln	Cys	Pro	
		355					360					365				
Leu	Leu	Arg	Arg	Gly	Leu	Asn	Tyr	Ile	Ile	Met	Gly	Gln	Val	Gly	Glu	
	370					375					380					
Asp	Gly	Arg	Gly	Lys	Ile	Met	Pro	Asn	Ser	Phe	Ile	Met	Met	Phe	Lys	
385					390					395					400	
Thr	Lys	Asn	Gln	Lys	Leu	Leu	Asp	Ala	Leu	Lys	Asn	Lys	Gln	Cys		
			405						410					415		

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 105

ccgattcata gacctcgaga gt

22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac

22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108

<211> 1838

<212> DNA

<213> Homo sapiens

<400> 108

cggacgcgtg	ggcggacgcg	tgggcgggccc	acggcgccccg	cgggctggggg	cggtcgcttc	60
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aagggcctag	tcccagctgt	gctctggggc	ctcagcctct	tcctcaacct	cccaggacct	180
atctggctcc	agccctctcc	acctccccag	tcttctcccc	cgctcagcc	ccatccgtgt	240
catacctgcc	ggggactggg	tgacagcttt	aacaagggcc	tggagagAAC	catccgggac	300
aactttggag	gtggaaacac	tgctggggag	gaagagaatt	tgtccaaata	caaagacagt	360
gagacccgcc	tggtagaggt	gctggagggt	gtgtgcagca	agtcagactt	cgagtgccac	420
cgctgtctgg	agctgagtga	ggagctgggt	gagagctggg	ggtttcacaa	gcagcaggag	480
gccccggacc	tcttccagtg	gctgtgctca	gattccctga	agctctgctg	ccccgcaggc	540
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gggcagtgtg	aaggagaagg	gacacgaggg	ggcagcgggc	actgtgactg	ccaagccggc	660
tacgggggtg	aggcctgtgg	ccagtgtggc	cttggctact	ttgaggcaga	acgcaacgcc	720
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tcaaactgtt	tgcaatgcaa	gaagggctgg	gccctgcata	acctcaagtg	tgtagacatt	840
gatgagtgtg	gcacagaggg	agccaactgt	ggagctgacc	aattctgcgt	gaacactgag	900
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ggtcgctgta	agaagtgtag	ccctggctat	cagcaggtgg	gctccaagtg	tctcgatgtg	1020
gatgagtgtg	agacagaggt	gtgtccggga	gagaacaagc	agtgtgaaaa	caccgagggc	1080
ggttatcgct	gcattctgtc	cgagggtctac	aagcagatgg	aaggcatctg	tgtgaaggag	1140
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cagcagatgt tctttggcat catcatctgt gcactggcca cgctggctgc taagggcgac 1260
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<210> 109
<211> 420
<212> PRT
<213> Homo sapiens

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<400> 109

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Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
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Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20             25             30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35             40             45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50             55             60

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu
      65             70             75             80

Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
      85             90             95

Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
      100            105            110

Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
      115            120            125

Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
      130            135            140

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu
      145            150            155            160

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly
      165            170            175

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys
      180            185            190

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His
      195            200            205

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Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro
 210 215 220
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His
 225 230 235 240
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys
 245 250 255
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg
 260 265 270
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg
 275 280 285
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu
 290 295 300
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln
 305 310 315 320
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr
 325 330 335
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala
 340 345 350
 Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
 355 360 365
 Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
 370 375 380
 Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
 385 390 395 400
 Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
 405 410 415
 Ile Lys Gly Arg
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 110

cctggcctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga

50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac

22

<210> 113

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1461)..(1461)

<223> a, t, c or g

<400> 113

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cggggccgcc	ctgaccgggg	agcagctcct	gggcagcctg	ctgcggcagc	tgcagctcaa	180
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gcgcagcgcc	cgggcccggg	tgaccgtcga	gtggctgcgc	gtccgcgacg	acggctccaa	540
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cgagaactgg	gtgctggagc	ccccgggctt	cctggcttat	gagtgtgtgg	gcacctgccg	960
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aaagtcctcc accaccactc tggacctaag acctgggggtt aagtgtgggt tgtgcatccc 1560
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<210> 114
 <211> 366
 <212> PRT
 <213> Homo sapiens

<400> 114

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Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
 20 25 30

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
 35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
 50 55 60

Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
 65 70 75 80

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
 85 90 95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
 100 105 110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
 115 120 125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
 130 135 140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
 145 150 155 160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
 165 170 175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
 180 185 190

Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
 195 200 205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
 210 215 220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
 225 230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
 245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
275 280 285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
355 360 365

<210> 115
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 115
aggactgccca taacttgccct g 21

<210> 116
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 116
ataggagttg aagcagcgct gc 22

<210> 117
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 117
tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118
 <211> 1857
 <212> DNA
 <213> Homo sapiens

<400> 118
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 ctggcattgg gcagtggttac agtgactctt tctgaacctg aagtcagaat tcctgagaat 180
 aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtggaag 240
 tttgaccaag gagacaccac cagactcgtt tgctataata acaagatcac agcttcctat 300
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 tacacctggt tcaaagatgg gatagtgatg cctacgaatc caaaagcac ccgtgccttc 600
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 gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
 tcaaattgctg tcgcatgga agctgtggag cggaatgtgg gggctatcgt ggcagccgtc 780
 cttgtaacctg tgattctcct gggaatcttg gtttttggca tctgggttgc ctatagccga 840
 ggccactttg acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900
 agtgcccga gtgaaggaga attcaaacag acctcgtcat tcctgggtgtg agcctggctg 960
 gctcaccgcc tatcatctgc atttgcctta ctcaggtgct accggactct ggccccctgat 1020
 gtctgtagtt tcacaggatg ccttatttgt cttctacacc ccacagggcc ccctacttct 1080
 tcggatgtgt ttttaataat gtcagctatg tgccccatcc tccttcatgc cctccctccc 1140
 tttcctacca ctgctgagtg gcctggaact tgtttaaagt gtttattccc catttctttg 1200
 agggatcagg aaggaatcct gggtatgcc a ttgacttccc ttctaagtag acagcaaaaa 1260
 tggcgggggt cgcaggaatc tgcactcaac tgcccacctg gctggcaggg atctttgaat 1320
 aggtatcttg agcttggttc tgggctcttt ccttgtgtac tgacgaccag ggccagctgt 1380
 tctagagcgg gaattagagg ctagagcggc tgaaatggtt gtttggtgat gacactgggg 1440
 tccttccatc tctggggccc actctcttct gtcttcccat gggaagtgcc actgggatcc 1500
 ctctgccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560
 agctcttggt gtggagagca tagtaaattt tcagagaact tgaagccaaa aggattttaa 1620
 accgctgtc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680
 cagaggctga ggcaggcgga tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
 ggagaaacct tactggaaat acaaagttag ccaggcatgg tgggtcatgc ctgtagtccc 1800
 agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

<210> 119
 <211> 299
 <212> PRT
 <213> Homo sapiens

<400> 119
 Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
 1 5 10 15
 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
 20 25 30
 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
 35 40 45
 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
 50 55 60

Asp	Gln	Gly	Asp	Thr	Thr	Arg	Leu	Val	Cys	Tyr	Asn	Asn	Lys	Ile	Thr	65	70	75	80
Ala	Ser	Tyr	Glu	Asp	Arg	Val	Thr	Phe	Leu	Pro	Thr	Gly	Ile	Thr	Phe	85	90	95	
Lys	Ser	Val	Thr	Arg	Glu	Asp	Thr	Gly	Thr	Tyr	Thr	Cys	Met	Val	Ser	100	105	110	
Glu	Glu	Gly	Gly	Asn	Ser	Tyr	Gly	Glu	Val	Lys	Val	Lys	Leu	Ile	Val	115	120	125	
Leu	Val	Pro	Pro	Ser	Lys	Pro	Thr	Val	Asn	Ile	Pro	Ser	Ser	Ala	Thr	130	135	140	
Ile	Gly	Asn	Arg	Ala	Val	Leu	Thr	Cys	Ser	Glu	Gln	Asp	Gly	Ser	Pro	145	150	155	160
Pro	Ser	Glu	Tyr	Thr	Trp	Phe	Lys	Asp	Gly	Ile	Val	Met	Pro	Thr	Asn	165	170	175	
Pro	Lys	Ser	Thr	Arg	Ala	Phe	Ser	Asn	Ser	Ser	Tyr	Val	Leu	Asn	Pro	180	185	190	
Thr	Thr	Gly	Glu	Leu	Val	Phe	Asp	Pro	Leu	Ser	Ala	Ser	Asp	Thr	Gly	195	200	205	
Glu	Tyr	Ser	Cys	Glu	Ala	Arg	Asn	Gly	Tyr	Gly	Thr	Pro	Met	Thr	Ser	210	215	220	
Asn	Ala	Val	Arg	Met	Glu	Ala	Val	Glu	Arg	Asn	Val	Gly	Val	Ile	Val	225	230	235	240
Ala	Ala	Val	Leu	Val	Thr	Leu	Ile	Leu	Leu	Gly	Ile	Leu	Val	Phe	Gly	245	250	255	
Ile	Trp	Phe	Ala	Tyr	Ser	Arg	Gly	His	Phe	Asp	Arg	Thr	Lys	Lys	Gly	260	265	270	
Thr	Ser	Ser	Lys	Lys	Val	Ile	Tyr	Ser	Gln	Pro	Ser	Ala	Arg	Ser	Glu	275	280	285	
Gly	Glu	Phe	Lys	Gln	Thr	Ser	Ser	Phe	Leu	Val						290	295		

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

<210> 121
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 121
 tgatcgcat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50

 <210> 122
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 122
 acacctggtt caaagatggg 20

 <210> 123
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 123
 taggaagagt tgctgaaggc acgg 24

 <210> 124
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 124
 ttgccttact caggtgctac 20

 <210> 125
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 125
actcagcagt ggtaggaaag

20

<210> 126
<211> 1210
<212> DNA
<213> Homo sapiens

<400> 126
cagcgcgtgg cccggcgccgc tgtggggaca gcatgagcgg cggttggatg ggcaggttg 60
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctcggactag 120
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgc 300
ggattgagcc atgtaccag aaagggcaat gcccaccgcc ccctggcctc ccctgcccct 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480
ggcgtgcga cggccacca gactgtccc actccagcga cgagctcggc tgtggaacca 540
atgagatcct cccggaagg gatgccaaa ccatggggcc ccctgtgacc ctggagagt 600
tcacctctct caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtcccct 660
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tggaagcca actgcctatg 720
gggttattgc agctgctgcg gtgctcagtg caagcctggt caccgccacc ctccctcttt 780
tgtcctggct ccgagcccag gagcgccctc gccactggg gttactggtg gccatgaagg 840
agtccctgct gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900
ccgtcactca gccctgggag tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960
gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaaccggagc 1020
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agctaggatg gggaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140
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aagttgcttc 1210

<210> 127
<211> 282
<212> PRT
<213> Homo sapiens

<400> 127
Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
1 5 10 15
Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
20 25 30
Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
35 40 45
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
50 55 60
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
65 70 75 80
Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
85 90 95
Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
 115 120 125
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
 130 135 140
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
 145 150 155 160
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
 165 170 175
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
 180 185 190
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
 195 200 205
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
 210 215 220
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala
 225 230 235 240
 Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln
 245 250 255
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
 260 265 270
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
 275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

24

<210> 129

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 129

ttggttcac agccgagctc gtcg

24

<210> 130
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 130
gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50

<210> 131
<211> 1843
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1837)..(1837)
<223> a, t, c or g

<400> 131
cccacgcgtc cgggtctcgtc cgctcgcgca gcgggcggcag cagagggtcgc gcacagatgc 60
gggttagact ggcgggggga ggaggcggag gaggggaagga agctgcatgc atgagacca 120
cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaacccga 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
gactcttggc cgtgatcctg tggtttcagc tggcgctgtg cttcggccct gcacagctca 300
cgggcggggt cgatgacctt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360
ggacccccag cggagggggt ttctttgaag gctctgtagc ccgattttcac tgccaagacg 420
gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcatttttaat ggaaccctag 480
gctggatccc aagtataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaactc 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgtc 600
atgaaggatt caagatccgg taccgccacc tacacaatat ggtttcatta tgtcgcgatg 660
atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780
atcgctgctt tcccgattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840
ttatctgggt gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900
ctccaatggt gagtcacgga gatttcgtct gccaccgcg gccttgtgag cgctacaacc 960
acggaactgt ggtggagttt tactgcgatc ctggctacag cctcaccagc gactacaagt 1020
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agcaaactg gccagcacc catgagacc tcctgaccac gtggaagatt gtggcggttca 1140
cggcaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200
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ttgtgggtgt agacggcgtg cccgtcatgc tcccgctcta tgacgaagct gtgagtggcg 1320
gcttgagtgc cttaggcccc gggtagatgg cctctgtggg ccagggtgc cccttaccg 1380
tggaagacca gagccccca gcatacccg gctcagggga cacggacaca ggcccagggg 1440
agtcagaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500
ctcccagggt ccaagagagc accaccctg cttcggacaa ccctgacata attgccagca 1560
cggcagagga ggtggcatcc accagcccag gcattccatca tgcccactgg gtgttgttcc 1620
taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680
gttgatctgt ggagttgatt ctttctcttc tcttggtttt agacaaatgt aaacaaagt 1740
ctgatcctta aaattgctat gctgatagag tggtaggggc tggaagcttg atcaagtcct 1800
gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met	Tyr	His	Gly	Met	Asn	Pro	Ser	Asn	Gly	Asp	Gly	Phe	Leu	Glu	Gln	
1				5					10					15		
Gln	Gln	Gln	Gln	Gln	Gln	Pro	Gln	Ser	Pro	Gln	Arg	Leu	Leu	Ala	Val	
			20					25					30			
Ile	Leu	Trp	Phe	Gln	Leu	Ala	Leu	Cys	Phe	Gly	Pro	Ala	Gln	Leu	Thr	
		35					40					45				
Gly	Gly	Phe	Asp	Asp	Leu	Gln	Val	Cys	Ala	Asp	Pro	Gly	Ile	Pro	Glu	
	50					55					60					
Asn	Gly	Phe	Arg	Thr	Pro	Ser	Gly	Gly	Val	Phe	Phe	Glu	Gly	Ser	Val	
65					70					75					80	
Ala	Arg	Phe	His	Cys	Gln	Asp	Gly	Phe	Lys	Leu	Lys	Gly	Ala	Thr	Lys	
				85					90						95	
Arg	Leu	Cys	Leu	Lys	His	Phe	Asn	Gly	Thr	Leu	Gly	Trp	Ile	Pro	Ser	
			100					105					110			
Asp	Asn	Ser	Ile	Cys	Val	Gln	Glu	Asp	Cys	Arg	Ile	Pro	Gln	Ile	Glu	
		115					120					125				
Asp	Ala	Glu	Ile	His	Asn	Lys	Thr	Tyr	Arg	His	Gly	Glu	Lys	Leu	Ile	
	130					135					140					
Ile	Thr	Cys	His	Glu	Gly	Phe	Lys	Ile	Arg	Tyr	Pro	Asp	Leu	His	Asn	
145					150					155					160	
Met	Val	Ser	Leu	Cys	Arg	Asp	Asp	Gly	Thr	Trp	Asn	Asn	Leu	Pro	Ile	
			165						170					175		
Cys	Gln	Gly	Cys	Leu	Arg	Pro	Leu	Ala	Ser	Ser	Asn	Gly	Tyr	Val	Asn	
			180					185					190			
Ile	Ser	Glu	Leu	Gln	Thr	Ser	Phe	Pro	Val	Gly	Thr	Val	Ile	Ser	Tyr	
		195					200					205				
Arg	Cys	Phe	Pro	Gly	Phe	Lys	Leu	Asp	Gly	Ser	Ala	Tyr	Leu	Glu	Cys	
	210					215					220					
Leu	Gln	Asn	Leu	Ile	Trp	Ser	Ser	Ser	Pro	Pro	Arg	Cys	Leu	Ala	Leu	
225					230					235					240	
Glu	Ala	Gln	Val	Cys	Pro	Leu	Pro	Pro	Met	Val	Ser	His	Gly	Asp	Phe	
				245					250					255		
Val	Cys	His	Pro	Arg	Pro	Cys	Glu	Arg	Tyr	Asn	His	Gly	Thr	Val	Val	
			260					265					270			
Glu	Phe	Tyr	Cys	Asp	Pro	Gly	Tyr	Ser	Leu	Thr	Ser	Asp	Tyr	Lys	Tyr	

275					280					285					
Ile	Thr	Cys	Gln	Tyr	Gly	Glu	Trp	Phe	Pro	Ser	Tyr	Gln	Val	Tyr	Cys
290					295					300					
Ile	Lys	Ser	Glu	Gln	Thr	Trp	Pro	Ser	Thr	His	Glu	Thr	Leu	Leu	Thr
305					310					315					
Thr	Trp	Lys	Ile	Val	Ala	Phe	Thr	Ala	Thr	Ser	Val	Leu	Leu	Val	Leu
325					330					335					
Leu	Leu	Val	Ile	Leu	Ala	Arg	Met	Phe	Gln	Thr	Lys	Phe	Lys	Ala	His
340					345					350					
Phe	Pro	Pro	Arg	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Ser	Asp	Pro	Asp	Phe
355					360					365					
Val	Val	Val	Asp	Gly	Val	Pro	Val	Met	Leu	Pro	Ser	Tyr	Asp	Glu	Ala
370					375					380					
Val	Ser	Gly	Gly	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Tyr	Met	Ala	Ser	Val
385					390					395					
Gly	Gln	Gly	Cys	Pro	Leu	Pro	Val	Asp	Asp	Gln	Ser	Pro	Pro	Ala	Tyr
405					410					415					
Pro	Gly	Ser	Gly	Asp	Thr	Asp	Thr	Gly	Pro	Gly	Glu	Ser	Glu	Thr	Cys
420					425					430					
Asp	Ser	Val	Ser	Gly	Ser	Ser	Glu	Leu	Leu	Gln	Ser	Leu	Tyr	Ser	Pro
435					440					445					
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile
450					455					460					
Ile	Ala	Ser	Thr	Ala	Glu	Glu	Val	Ala	Ser	Thr	Ser	Pro	Gly	Ile	His
465					470					475					
His	Ala	His	Trp	Val	Leu	Phe	Leu	Arg	Asn						
485					490										

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttaca aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc	cgctccgcgc	cctccccccc	gcctcccgtg	cggctccgtc	gtggcctaga	60
gatgctgctg	ccgcggttgc	agttgtcgcg	cacgcctctg	cccgccagcc	cgctccaccg	120
ccgtagcgcc	cgagtgtcgg	ggggcgcacc	cgagtccggc	catgaggccg	ggaaccgcgc	180
tacaggccgt	gctgctggcc	gtgctgctgg	tggggctgcg	ggccgcgacg	ggtcgcctgc	240
tgagtgcctc	ggatttggac	ctcagaggag	ggcagccagt	ctgccgggga	gggacacaga	300
ggccttgтта	taaagtcatt	tacttccatg	atacttctcg	aagactgaac	tttgagggaag	360
ccaaagaagc	ctgcaggagg	gatggaggcc	agctagtcat	catcgagtct	gaagatgaac	420
agaaactgat	agaaaagttc	attgaaaacc	tcttgccatc	tgatgggtgac	ttctggattg	480
ggctcaggag	gcgtgaggag	aaacaaagca	atagcacagc	ctgccaggac	ctttatgctt	540
ggactgatgg	cagcatatca	caatttagga	actggtatgt	ggatgagccg	tcctgcggca	600
gcgaggctcg	cgtggtcatg	taccatcagc	catcggcacc	cgctggcatc	ggaggccctt	660
acatgttcca	gtggaatgat	gaccggtgca	acatgaagaa	caatttcatt	tgcaaatatt	720
ctgatgagaa	accagcagtt	ccttctagag	aagctgaagg	tgaggaaaca	gagctgacaa	780
cacctgtact	tccagaagaa	acacaggaag	aagatgccaa	aaaaacattt	aaagaaagta	840
gagaagctgc	cttgaatctg	gcctacatcc	taatccccag	cattccccct	ctcctcctcc	900
ttgtggtcac	cacagtgtga	tgttgggttt	ggatctgtag	aaaaagaaaa	cgggagcagc	960
cagaccctag	cacaaagaag	caacacacca	tctggccctc	tcctcaccag	ggaaacagcc	1020
cggacctaga	ggtctacaat	gtcataagaa	aacaaagcga	agctgactta	gctgagaccc	1080
ggccagacct	gaagaatatt	tcattccgag	tgtgttcggg	agaagccact	cccgatgaca	1140
tgtcttgtga	ctatgacaac	atggctgtga	acccatcaga	aagtgggttt	gtgactctgg	1200
tgagcgtgga	gagtggattt	gtgaccaatg	acatttatga	gttctcccca	gaccaaattg	1260
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aaactgaaac	tgacaacaat	ggaaaagaaa	tgataagcaa	aatcctctta	ttttctataa	1380
ggaaaataca	cagaaggtct	atgaacaagc	ttagatcagg	tcctgtggat	gagcatgtgg	1440
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aaatgtcact	tggttggttg	tatctaactt	ttaagggaca	gagctttacc	tggcagtgat	1620
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atattatcat	acagacagaa	aatccagaat	cttttcaaag	cccacatatg	gtagcacagg	1740
ttggcctgtg	catcggcaat	tctcatatct	gtttttttca	aagaataaaa	tcaaataaag	1800
agcaggaaaa	aaaaaa					1815

<400> 140
cagtccaagc ataaagggtcc tggc 24

<210> 141
 <211> 1514
 <212> DNA
 <213> Homo sapiens

<400> 141
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60
 gcatccgcag gttcccgcgg acttgggggc gcccgtgag ccccggcgcc cgcagaagac 120
 ttgtgtttgc ctccctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgtc ctgacctcgc tggcgtactg 240
 cctgcaccag cggcgggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg tttcgacacg gggctcggag 360
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaccata 480
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540
 gctgaccaag gtgggcatgc agcaaagtgt tgccttgga gagagactga ggaagaacta 600
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 cactaacatt tttcggaatc tggagtccac ccgttgtttg ctggctgggc ttttccagtg 720
 tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgtatcc 780
 caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
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 tagtgataaa gtggacttct tcctcctcct ggacaacgtg gctgccgagc aggcacacaa 960
 cctcccaagc tgcccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020
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 attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140
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 agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440
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 gcctttatac aatg 1514

<210> 142
 <211> 428
 <212> PRT
 <213> Homo sapiens

<400> 142
 Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
 1 5 10 15
 Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
 20 25 30
 Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
 35 40 45
 Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
 50 55 60
 Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
 65 70 75 80
 Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
 85 90 95

Ala	Gly	Gly	Pro	Lys	Pro	Tyr	Ser	Pro	Tyr	Asp	Ser	Gln	Tyr	His	Glu	
			100					105					110			
Thr	Thr	Leu	Lys	Gly	Gly	Met	Phe	Ala	Gly	Gln	Leu	Thr	Lys	Val	Gly	
		115					120					125				
Met	Gln	Gln	Met	Phe	Ala	Leu	Gly	Glu	Arg	Leu	Arg	Lys	Asn	Tyr	Val	
	130					135					140					
Glu	Asp	Ile	Pro	Phe	Leu	Ser	Pro	Thr	Phe	Asn	Pro	Gln	Glu	Val	Phe	
145					150					155					160	
Ile	Arg	Ser	Thr	Asn	Ile	Phe	Arg	Asn	Leu	Glu	Ser	Thr	Arg	Cys	Leu	
				165					170					175		
Leu	Ala	Gly	Leu	Phe	Gln	Cys	Gln	Lys	Glu	Gly	Pro	Ile	Ile	Ile	His	
			180					185					190			
Thr	Asp	Glu	Ala	Asp	Ser	Glu	Val	Leu	Tyr	Pro	Asn	Tyr	Gln	Ser	Cys	
	195						200					205				
Trp	Ser	Leu	Arg	Gln	Arg	Thr	Arg	Gly	Arg	Arg	Gln	Thr	Ala	Ser	Leu	
	210					215					220					
Gln	Pro	Gly	Ile	Ser	Glu	Asp	Leu	Lys	Lys	Val	Lys	Asp	Arg	Met	Gly	
225					230					235					240	
Ile	Asp	Ser	Ser	Asp	Lys	Val	Asp	Phe	Phe	Ile	Leu	Leu	Asp	Asn	Val	
				245					250					255		
Ala	Ala	Glu	Gln	Ala	His	Asn	Leu	Pro	Ser	Cys	Pro	Met	Leu	Lys	Arg	
			260					265					270			
Phe	Ala	Arg	Met	Ile	Glu	Gln	Arg	Ala	Val	Asp	Thr	Ser	Leu	Tyr	Ile	
	275						280					285				
Leu	Pro	Lys	Glu	Asp	Arg	Glu	Ser	Leu	Gln	Met	Ala	Val	Gly	Pro	Phe	
	290					295					300					
Leu	His	Ile	Leu	Glu	Ser	Asn	Leu	Leu	Lys	Ala	Met	Asp	Ser	Ala	Thr	
305					310					315					320	
Ala	Pro	Asp	Lys	Ile	Arg	Lys	Leu	Tyr	Leu	Tyr	Ala	Ala	His	Asp	Val	
				325					330					335		
Thr	Phe	Ile	Pro	Leu	Leu	Met	Thr	Leu	Gly	Ile	Phe	Asp	His	Lys	Trp	
			340					345					350			
Pro	Pro	Phe	Ala	Val	Asp	Leu	Thr	Met	Glu	Leu	Tyr	Gln	His	Leu	Glu	
		355					360					365				
Ser	Lys	Glu	Trp	Phe	Val	Gln	Leu	Tyr	Tyr	His	Gly	Lys	Glu	Gln	Val	
	370					375					380					
Pro	Arg	Gly	Cys	Pro	Asp	Gly	Leu	Cys	Pro	Leu	Asp	Met	Phe	Leu	Asn	
385					390					395					400	

Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
405 410 415

Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
420 425

<210> 143
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 143
ccaactacca aagctgctgg agcc 24

<210> 144
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 144
gcagctctat taccacggga agga 24

<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 145
tccttcccgt ggtaatagag ctgc 24

<210> 146
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 146
ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg 45

<210> 147
<211> 1686

<212> DNA
<213> Homo sapiens

<400> 147

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ctcctctttaa cataacttgca gctaaaaacta aatattgctg cttgggggacc tccttctagc 60
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ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgtgg 300
agctgccagc ggaaccctta gtggtatttt gtatgagcca ccagcagaaa aagagcaaaa 360
ggctctcatc caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420
agaagaagtt tatgattgtt cacatgatga agatgctggg gcatcgtgtg agaaccaga 480
gagctctttc tccccagtcc cagaggggtgt caggctggct gacggccctg ggcattgcaa 540
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600
cctccggggc gcaaagggtg tgtgccggca gctgggatgt gggagggtct tactgactca 660
aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggctgagcc agatgtcatg 720
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caacctgatg gaagacacgt gggctcgaatg tgaagatccc tttgacttga gactagtagg 840
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tccacattgc acacagcaga ttcccagcct ccataattgt gtgtatcaac tacttaaata 1440
cattctcaca cacacacaca cacacacaca cacacacaca cacacataca ccatttgtcc 1500
tgtttctctg aagaactctg acaaaaataca gattttggta ctgaaagaga ttctagagga 1560
acggaatttt aaggataaat tttctgaatt ggttatgggg tttctgaaat tggctctata 1620
atctaattag atataaaatt ctggtaactt tattttacaat aataaagata gcactatgtg 1680
ttcaaa 1686
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<210> 148
<211> 347
<212> PRT
<213> Homo sapiens

<400> 148

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Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
  1             5             10             15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
      20             25             30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
      35             40             45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
      50             55             60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
      65             70             75             80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
      85             90             95
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Thr	Gly	Thr	Glu	Asp	Thr	Leu	Ala	Gln	Cys	Glu	Gln	Glu	Glu	Val	Tyr	
			100					105					110			
Asp	Cys	Ser	His	Asp	Glu	Asp	Ala	Gly	Ala	Ser	Cys	Glu	Asn	Pro	Glu	
		115					120					125				
Ser	Ser	Phe	Ser	Pro	Val	Pro	Glu	Gly	Val	Arg	Leu	Ala	Asp	Gly	Pro	
	130					135					140					
Gly	His	Cys	Lys	Gly	Arg	Val	Glu	Val	Lys	His	Gln	Asn	Gln	Trp	Tyr	
145					150					155					160	
Thr	Val	Cys	Gln	Thr	Gly	Trp	Ser	Leu	Arg	Ala	Ala	Lys	Val	Val	Cys	
				165					170					175		
Arg	Gln	Leu	Gly	Cys	Gly	Arg	Ala	Val	Leu	Thr	Gln	Lys	Arg	Cys	Asn	
		180						185					190			
Lys	His	Ala	Tyr	Gly	Arg	Lys	Pro	Ile	Trp	Leu	Ser	Gln	Met	Ser	Cys	
	195						200					205				
Ser	Gly	Arg	Glu	Ala	Thr	Leu	Gln	Asp	Cys	Pro	Ser	Gly	Pro	Trp	Gly	
	210					215					220					
Lys	Asn	Thr	Cys	Asn	His	Asp	Glu	Asp	Thr	Trp	Val	Glu	Cys	Glu	Asp	
225					230					235					240	
Pro	Phe	Asp	Leu	Arg	Leu	Val	Gly	Gly	Asp	Asn	Leu	Cys	Ser	Gly	Arg	
			245						250					255		
Leu	Glu	Val	Leu	His	Lys	Gly	Val	Trp	Gly	Ser	Val	Cys	Asp	Asp	Asn	
			260					265					270			
Trp	Gly	Glu	Lys	Glu	Asp	Gln	Val	Val	Cys	Lys	Gln	Leu	Gly	Cys	Gly	
	275						280					285				
Lys	Ser	Leu	Ser	Pro	Ser	Phe	Arg	Asp	Arg	Lys	Cys	Tyr	Gly	Pro	Gly	
	290					295					300					
Val	Gly	Arg	Ile	Trp	Leu	Asp	Asn	Val	Arg	Cys	Ser	Gly	Glu	Glu	Gln	
305					310					315					320	
Ser	Leu	Glu	Gln	Cys	Gln	His	Arg	Phe	Trp	Gly	Phe	His	Asp	Cys	Thr	
				325					330					335		
His	Gln	Glu	Asp	Val	Ala	Val	Ile	Cys	Ser	Val						
			340					345								

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 149
ttcagctcat caccttcacc tgcc 24

<210> 150
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 150
ggctcataca aaataccact aggg 24

<210> 151
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 151
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt 50

<210> 152
<211> 1427
<212> DNA
<213> Homo sapiens

<400> 152
actgcactcg gttctatcga ttgaattccc cgggggatcct ctagagatcc ctcgacctcg 60
accacgcgt ccgcggacgc gtgggcccgc gctggggccg gctaccagga agagtctgcc 120
gaaggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180
cctgggcgtc ttcggcctct tccggctgct gcagtggtg cgcggaagg cctacctgcg 240
gaatgctgtg gtggtgatca caggcgccac ctcagggtcg ggcaaagaat gtgcaaaagt 300
cttctatgct gcgggtgcta aactggtgct ctgtggcccg aatggtgggg ccctagaaga 360
gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420
ggtgaccttc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480
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catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600
tgctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660
catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720
gcacgcaacc caggctttct ttgactgtct gcgtgcccag atggaacagt atgaaattga 780
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gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc caggggtgagg 1260
ggaaacactt aaggataaaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380

cttgcccgcc atggcccaac ttgtttattg cagcttataa tggttac

1427

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
20 25 30

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr
210 215 220

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg
225 230 235 240

Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu
245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val

260	265	270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
275	280	285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
290	295	300
Arg Lys Ser Lys Asn Ser		
305	310	

<210> 154
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 154
 ggtgctaaac tgggtgctctg tggc 24

<210> 155
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 155
 cagggcaaga tgagcattcc 20

<210> 156
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 156
 tcatactgtt ccatctcggc acgc 24

<210> 157
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 157

aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc

50

<210> 158

<211> 1771

<212> DNA

<213> Homo sapiens

<400> 158

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cccacgcgtc cgctgggtgtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60
aaaaaaaaaa acacacccaaa cgctcgcagc cacaaaaggg atgaaatttc ttctggacat 120
cctcctgctt ctcccggttac tgatcgtctg ctccctagag tccttcgtga agctttttat 180
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcatgg 240
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg gtgccaaggt 360
tcataccttt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420
gaaggcagaa attggagatg ttagtatttt agtaaataat gctgggttag tctatacatc 480
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acatttctgg actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600
tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg cttactgttc 660
aagcaagttt gctgctgttg gatctcataa aactttgaca gatgaactgg ctgccttaca 720
aataactgga gtcaaaaacaa catgtctgtg tcctaatttc gtaaactg gcttcatcaa 780
aaatccaagt acaagtttgg gaccactctt ggaacctgag gaagtggtaa acaggctgat 840
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aactgattta ccaggttttag gttgatgtca tctaatagtg ccagaatttt aatgtttgaa 1080
cttctgtttt ttctaattat cccatttctt tcaatatcat ttttgaggct ttggcagtct 1140
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agagaatgta ccacaaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a aaaaaaaaaa 1771
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<210> 159

<211> 300

<212> PRT

<213> Homo sapiens

<400> 159

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Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile Val
 1                      5                      10                      15

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys
                20                      25                      30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
                35                      40                      45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
 50                      55                      60
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Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	Thr	Ala	Ala	Lys	Cys	
65					70					75					80	
Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	Val	Val	Asp	Cys	Ser	Asn	
				85					90					95		
Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	Lys	Val	Lys	Ala	Glu	Ile	Gly	
			100					105					110			
Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp	
		115					120					125				
Leu	Phe	Ala	Thr	Gln	Asp	Pro	Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn	
	130					135					140					
Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr	
145					150					155					160	
Lys	Asn	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His	
				165					170					175		
Val	Ser	Val	Pro	Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	
			180					185					190			
Val	Gly	Phe	His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile	
		195					200					205				
Thr	Gly	Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn	Phe	Val	Asn	Thr	Gly	
	210					215					220					
Phe	Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly	Pro	Thr	Leu	Glu	Pro	Glu	
225					230					235					240	
Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly	Ile	Leu	Thr	Glu	Gln	Lys	Met	
				245					250					255		
Ile	Phe	Ile	Pro	Ser	Ser	Ile	Ala	Phe	Leu	Thr	Thr	Leu	Glu	Arg	Ile	
			260					265					270			
Leu	Pro	Glu	Arg	Phe	Leu	Ala	Val	Leu	Lys	Arg	Lys	Ile	Ser	Val	Lys	
		275					280					285				
Phe	Asp	Ala	Val	Ile	Gly	Tyr	Lys	Met	Lys	Ala	Gln					
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<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 160

ggatgaaggca gaaattggag atg

<210> 161
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 161
atcccatgca tcagcctggt tacc 24

<210> 162
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 162
gctgggtgtag tctatacatc agatttggtt gctacacaag atcctcag 48

<210> 163
<211> 2076
<212> DNA
<213> Homo sapiens

<400> 163
cccacgcgtc cgcgagcgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60
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<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

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Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
      35              40              45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
      50              55              60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val
      65              70              75              80

Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln
      85              90              95

Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro
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Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val
      115             120             125

Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr
      130             135             140

Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser
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Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala
      165             170             175

Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu
      180             185             190

Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys
      195             200             205

Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg
      210             215             220

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Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser		
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Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile		
				245					250					255			
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His		
			260					265					270				
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu		
		275					280					285					
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr		
	290					295					300						
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys		
305					310					315					320		
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro		
				325					330						335		
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly		
			340					345					350				
Thr	Ile	Val	Glu	Lys	Tyr	Leu	Arg	Glu	Asp	Thr	Val	Gln	Ser	Val	Lys		
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Pro	Trp	Leu	Thr	Glu	Ile	Met	Asn	Asn	Tyr	Lys	Val	Leu	Ile	Tyr	Asn		
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Gly	Gln	Leu	Asp	Ile	Ile	Val	Ala	Ala	Ala	Leu	Thr	Glu	Arg	Ser	Leu		
385					390					395					400		
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Lys	Val	Trp	Lys	Ile	Phe	Lys	Ser	Asp	Ser	Glu	Val	Ala	Gly	Tyr	Ile		
			420					425					430				
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		435					440					445					
Ile	Leu	Pro	Tyr	Asp	Gln	Pro	Leu	Arg	Ala	Phe	Asp	Met	Ile	Asn	Arg		
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Phe	Ile	Tyr	Gly	Lys	Gly	Trp	Asp	Pro	Tyr	Val	Gly						
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<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 165
ttccatgccca cctaaggag actc 24

<210> 166
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 166
tggatgaggt gtgcaatggc tggc 24

<210> 167
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 167
agctctcaga ggctggtcat aggg 24

<210> 168
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 168
gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac 50

<210> 169
<211> 2477
<212> DNA
<213> Homo sapiens

<400> 169
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accaggatgg ggaccctggg tcaggccagc ctctttgctc ctcccggaaa ttatttttgg 720

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acatctgcaa aagcaaa 2477

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<210> 170
 <211> 552
 <212> PRT
 <213> Homo sapiens

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<400> 170
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Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
      20              25              30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
      35              40              45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
      50              55              60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
      65              70              75              80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
      85              90              95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
      100             105             110

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Thr	Gly	Ala	Val	Tyr	Val	Gly	Ala	Ile	Asn	Arg	Val	Tyr	Lys	Leu	Thr	115	120	125
Gly	Asn	Leu	Thr	Ile	Gln	Val	Ala	His	Lys	Thr	Gly	Pro	Glu	Glu	Asp	130	135	140
Asn	Lys	Ser	Arg	Tyr	Pro	Pro	Leu	Ile	Val	Gln	Pro	Cys	Ser	Glu	Val	145	150	155
Leu	Thr	Leu	Thr	Asn	Asn	Val	Asn	Lys	Leu	Leu	Ile	Ile	Asp	Tyr	Ser	165	170	175
Glu	Asn	Arg	Leu	Leu	Ala	Cys	Gly	Ser	Leu	Tyr	Gln	Gly	Val	Cys	Lys	180	185	190
Leu	Leu	Arg	Leu	Asp	Asp	Leu	Phe	Ile	Leu	Val	Glu	Pro	Ser	His	Lys	195	200	205
Lys	Glu	His	Tyr	Leu	Ser	Ser	Val	Asn	Lys	Thr	Gly	Thr	Met	Tyr	Gly	210	215	220
Val	Ile	Val	Arg	Ser	Glu	Gly	Glu	Asp	Gly	Lys	Leu	Phe	Ile	Gly	Thr	225	230	235
Ala	Val	Asp	Gly	Lys	Gln	Asp	Tyr	Phe	Pro	Thr	Leu	Ser	Ser	Arg	Lys	245	250	255
Leu	Pro	Arg	Asp	Pro	Glu	Ser	Ser	Ala	Met	Leu	Asp	Tyr	Glu	Leu	His	260	265	270
Ser	Asp	Phe	Val	Ser	Ser	Leu	Ile	Lys	Ile	Pro	Ser	Asp	Thr	Leu	Ala	275	280	285
Leu	Val	Ser	His	Phe	Asp	Ile	Phe	Tyr	Ile	Tyr	Gly	Phe	Ala	Ser	Gly	290	295	300
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Ala	Ile	Asn	Ser	Ala	Gly	Asp	Leu	Phe	Tyr	Thr	Ser	Arg	Ile	Val	Arg	325	330	335
Leu	Cys	Lys	Asp	Asp	Pro	Lys	Phe	His	Ser	Tyr	Val	Ser	Leu	Pro	Phe	340	345	350
Gly	Cys	Thr	Arg	Ala	Gly	Val	Glu	Tyr	Arg	Leu	Leu	Gln	Ala	Ala	Tyr	355	360	365
Leu	Ala	Lys	Pro	Gly	Asp	Ser	Leu	Ala	Gln	Ala	Phe	Asn	Ile	Thr	Ser	370	375	380
Gln	Asp	Asp	Val	Leu	Phe	Ala	Ile	Phe	Ser	Lys	Gly	Gln	Lys	Gln	Tyr	385	390	395
His	His	Pro	Pro	Asp	Asp	Ser	Ala	Leu	Cys	Ala	Phe	Pro	Ile	Arg	Ala	405	410	415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
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 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
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 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn
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 Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr
 465 470 475 480
 Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly
 485 490 495
 Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val
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 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys
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 Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln
 530 535 540
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 545 550

<210> 171
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 171
 tggaataccg cctcctgcag 20

<210> 172
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 172
 cttctgccct ttggagaaga tggc 24

<210> 173
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 173

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43

<210> 174

<211> 3106

<212> DNA

<213> Homo sapiens

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<222> (1683)..(1683)

<223> a, t, c or g

<400> 174

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<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (539)

<223> Any amino acid

<400> 175

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Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
  1             5             10             15

```

```

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
      20             25             30

```

```

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
    35             40             45

```

```

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
    50             55             60

```

```

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
    65             70             75             80

```

```

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
      85             90             95

```

```

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
    100            105            110

```

```

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
    115            120            125

```

```

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
    130            135            140

```

```

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
    145            150            155            160

```

```

Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp

```

165								170					175			
His	Leu	Met	Ser 180	Arg	Val	Val	Pro	Leu 185	Gln	Tyr	Lys	Arg	Gly 190	Gly	Pro	
Ile	Ile	Ala 195	Val	Gln	Val	Glu	Asn 200	Glu	Tyr	Gly	Ser	Tyr 205	Asn	Lys	Asp	
Pro	Ala 210	Tyr	Met	Pro	Tyr	Val 215	Lys	Lys	Ala	Leu	Glu 220	Asp	Arg	Gly	Ile	
Val 225	Glu	Leu	Leu	Leu	Thr 230	Ser	Asp	Asn	Lys	Asp 235	Gly	Leu	Ser	Lys	Gly 240	
Ile	Val	Gln	Gly	Val 245	Leu	Ala	Thr	Ile	Asn 250	Leu	Gln	Ser	Thr	His 255	Glu	
Leu	Gln	Leu	Leu 260	Thr	Thr	Phe	Leu	Phe 265	Asn	Val	Gln	Gly	Thr 270	Gln	Pro	
Lys	Met	Val 275	Met	Glu	Tyr	Trp	Thr 280	Gly	Trp	Phe	Asp	Ser 285	Trp	Gly	Gly	
Pro	His 290	Asn	Ile	Leu	Asp	Ser 295	Ser	Glu	Val	Leu	Lys 300	Thr	Val	Ser	Ala	
Ile 305	Val	Asp	Ala	Gly	Ser 310	Ser	Ile	Asn	Leu	Tyr 315	Met	Phe	His	Gly	Gly 320	
Thr	Asn	Phe	Gly	Phe 325	Met	Asn	Gly	Ala	Met 330	His	Phe	His	Asp	Tyr 335	Lys	
Ser	Asp	Val	Thr 340	Ser	Tyr	Asp	Tyr	Asp 345	Ala	Val	Leu	Thr	Glu 350	Ala	Gly	
Asp	Tyr	Thr 355	Ala	Lys	Tyr	Met	Lys 360	Leu	Arg	Asp	Phe	Phe 365	Gly	Ser	Ile	
Ser	Gly 370	Ile	Pro	Leu	Pro	Pro 375	Pro	Pro	Asp	Leu	Leu 380	Pro	Lys	Met	Pro	
Tyr 385	Glu	Pro	Leu	Thr	Pro 390	Val	Leu	Tyr	Leu	Ser 395	Leu	Trp	Asp	Ala	Leu 400	
Lys	Tyr	Leu	Gly	Glu 405	Pro	Ile	Lys	Ser	Glu 410	Lys	Pro	Ile	Asn	Met 415	Glu	
Asn	Leu	Pro	Val 420	Asn	Gly	Gly	Asn	Gly 425	Gln	Ser	Phe	Gly	Tyr 430	Ile	Leu	
Tyr	Glu	Thr 435	Ser	Ile	Thr	Ser	Ser 440	Gly	Ile	Leu	Ser	Gly 445	His	Val	His	
Asp	Arg 450	Gly	Gln	Val	Phe	Val 455	Asn	Thr	Val	Ser	Ile 460	Gly	Phe	Leu	Asp	
Tyr	Lys	Thr	Thr	Lys	Ile	Ala	Val	Pro	Leu	Ile	Gln	Gly	Tyr	Thr	Val	

465		470		475		480
Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn						
	485			490		495
Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp						
	500			505		510
Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser						
	515			520		525
Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr						
	530			535		540
Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr						
	545			550		555
Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val						
	565			570		575
Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln						
	580			585		590
Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln						
	595			600		605
Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr						
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Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys						
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<210> 176
 <211> 2505
 <212> DNA
 <213> Homo sapiens

<400> 176

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aaggggagca	aagccgggct	cggcccagag	ccccaggac	ctccatctcc	caatgtttgga	180
ggaatccgac	acgtgacggt	ctgtccgccg	tctcagacta	gaggagcgct	gtaaacgccca	240
tggctcccaa	gaagctgtcc	tgcttctcgt	ccctgctgct	gccgctcagc	ctgacgctac	300
tgctgcccc	ggcagacact	cggtcgttcg	tagtggatag	gggtcatgac	cggtttctcc	360
tagacggggc	cccgttccgc	tatgtgtctg	gcagcctgca	ctactttcgg	gtaccgcggg	420
tgctttgggc	cgaccggctt	ttgaagatgc	gatggagcgg	cctcaacgcc	atacagtttt	480
atgtgccctg	gaactaccac	gagccacagc	ctgggggtcta	taactttaat	ggcagccggg	540
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gaccttacat	ctgtgcagag	tgggagatgg	ggggtctccc	atcctgggtg	cttcgaaaac	660
ctgaaattca	tctaagaacc	tcagatccag	acttccttgc	cgcagtggac	tcctggttca	720
aggtcttgct	gccaagata	tatccatggc	tttatcacia	tgggggcaac	atcattagca	780
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tggctgggct	cttccgtgca	ctgctaggag	aaaagatctt	gctcttcacc	acagatgggc	900
ctgaaggact	caagtgtggc	tccctccggg	gactctatac	cactgtagat	tttggcccag	960
ctgacaacat	gacaaaaatc	tttaccctgc	ttcgggaagta	tgaaccccat	gggccattgg	1020
taaaactctga	gtactacaca	ggctggctgg	attactgggg	ccagaatcac	tccacacggg	1080
ctgtgtcagc	tgtaaccaaa	ggactagaga	acatgctcaa	gttgggagcc	agtgtgaaca	1140

```

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gcttccttcc gattactacc agctatgact atgatgcacc tatatctgaa gcaggggacc 1260
ccacacctaa gctttttgct cttcgagatg tcatcagcaa gttccaggaa gttccttttg 1320
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<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

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Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
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Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
          20              25              30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
  35              40              45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
  50              55              60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe
  65              70              75              80

Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe
          85              90              95

Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala
          100              105              110

Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp
          115              120              125

Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His
          130              135              140

```

Leu	Arg	Thr	Ser	Asp	Pro	Asp	Phe	Leu	Ala	Ala	Val	Asp	Ser	Trp	Phe	
145					150					155					160	
Lys	Val	Leu	Leu	Pro	Lys	Ile	Tyr	Pro	Trp	Leu	Tyr	His	Asn	Gly	Gly	
				165					170					175		
Asn	Ile	Ile	Ser	Ile	Gln	Val	Glu	Asn	Glu	Tyr	Gly	Ser	Tyr	Arg	Ala	
			180					185					190			
Cys	Asp	Phe	Ser	Tyr	Met	Arg	His	Leu	Ala	Gly	Leu	Phe	Arg	Ala	Leu	
		195					200					205				
Leu	Gly	Glu	Lys	Ile	Leu	Leu	Phe	Thr	Thr	Asp	Gly	Pro	Glu	Gly	Leu	
	210					215					220					
Lys	Cys	Gly	Ser	Leu	Arg	Gly	Leu	Tyr	Thr	Thr	Val	Asp	Phe	Gly	Pro	
225					230					235					240	
Ala	Asp	Asn	Met	Thr	Lys	Ile	Phe	Thr	Leu	Leu	Arg	Lys	Tyr	Glu	Pro	
				245					250					255		
His	Gly	Pro	Leu	Val	Asn	Ser	Glu	Tyr	Tyr	Thr	Gly	Trp	Leu	Asp	Tyr	
			260					265					270			
Trp	Gly	Gln	Asn	His	Ser	Thr	Arg	Ser	Val	Ser	Ala	Val	Thr	Lys	Gly	
		275					280					285				
Leu	Glu	Asn	Met	Leu	Lys	Leu	Gly	Ala	Ser	Val	Asn	Met	Tyr	Met	Phe	
	290					295					300					
His	Gly	Gly	Thr	Asn	Phe	Gly	Tyr	Trp	Asn	Gly	Ala	Asp	Lys	Lys	Gly	
305					310					315					320	
Arg	Phe	Leu	Pro	Ile	Thr	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Ile	Ser	
				325					330					335		
Glu	Ala	Gly	Asp	Pro	Thr	Pro	Lys	Leu	Phe	Ala	Leu	Arg	Asp	Val	Ile	
			340					345					350			
Ser	Lys	Phe	Gln	Glu	Val	Pro	Leu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Pro	
		355					360					365				
Lys	Met	Met	Leu	Gly	Pro	Val	Thr	Leu	His	Leu	Val	Gly	His	Leu	Leu	
	370					375					380					
Ala	Phe	Leu	Asp	Leu	Leu	Cys	Pro	Arg	Gly	Pro	Ile	His	Ser	Ile	Leu	
385					390					395					400	
Pro	Met	Thr	Phe	Glu	Ala	Val	Lys	Gln	Asp	His	Gly	Phe	Met	Leu	Tyr	
				405					410					415		
Arg	Thr	Tyr	Met	Thr	His	Thr	Ile	Phe	Glu	Pro	Thr	Pro	Phe	Trp	Val	
			420					425					430			
Pro	Asn	Asn	Gly	Val	His	Asp	Arg	Ala	Tyr	Val	Met	Val	Asp	Gly	Val	
		435					440					445				

Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr
 450 455 460
 Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg
 465 470 475 480
 Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro
 485 490 495
 Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu
 500 505 510
 Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys
 515 520 525
 Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr
 530 535 540
 Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly
 545 550 555 560
 Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr
 565 570 575
 Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu
 580 585 590
 Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu
 595 600 605
 Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu
 610 615 620
 Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
 625 630 635 640
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 645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 178

tggtactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 179

tggacaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttatatt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22

<210> 182

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 182

tggcacccag aatggtgttg gctc

24

<210> 183

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 183

cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc

50

<210> 184

<211> 1947

<212> DNA

<213> Homo sapiens

<400> 184

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gtgtttatgg ctttatctgc ctctacactc tcttctggtt attcaggata cttttgaagg 180
aatattcttt cgaaaaagtc agagaagaga gcagtttttag tgacattcca gatgtcaaaa 240
acgattttgc gttccttctt cacatggttag accagtatga ccagctatat tccaagcgtt 300
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cctgggtgta tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720
aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780
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ttttcttact aaaaaaaaaa aaaaaaa 1947
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<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

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  20             25             30

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
  35             40             45

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
  50             55             60

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
  65             70             75             80
```

Leu	Ser	Glu	Val	Ser	Glu	Asn	Lys	Leu	Arg	Glu	Ile	Ser	Leu	Asn	His	
				85					90					95		
Glu	Trp	Thr	Phe	Glu	Lys	Leu	Arg	Gln	His	Ile	Ser	Arg	Asn	Ala	Gln	
			100					105					110			
Asp	Lys	Gln	Glu	Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Val	Pro	Asp	Ala	
		115					120					125				
Val	Phe	Asp	Leu	Thr	Asp	Leu	Asp	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro	
	130					135					140					
Glu	Ala	Lys	Ile	Pro	Ala	Lys	Ile	Ser	Gln	Met	Thr	Asn	Leu	Gln	Glu	
145					150					155					160	
Leu	His	Leu	Cys	His	Cys	Pro	Ala	Lys	Val	Glu	Gln	Thr	Ala	Phe	Ser	
			165						170					175		
Phe	Leu	Arg	Asp	His	Leu	Arg	Cys	Leu	His	Val	Lys	Phe	Thr	Asp	Val	
			180					185					190			
Ala	Glu	Ile	Pro	Ala	Trp	Val	Tyr	Leu	Leu	Lys	Asn	Leu	Arg	Glu	Leu	
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Tyr	Leu	Ile	Gly	Asn	Leu	Asn	Ser	Glu	Asn	Asn	Lys	Met	Ile	Gly	Leu	
	210					215					220					
Glu	Ser	Leu	Arg	Glu	Leu	Arg	His	Leu	Lys	Ile	Leu	His	Val	Lys	Ser	
225					230					235					240	
Asn	Leu	Thr	Lys	Val	Pro	Ser	Asn	Ile	Thr	Asp	Val	Ala	Pro	His	Leu	
			245						250				255			
Thr	Lys	Leu	Val	Ile	His	Asn	Asp	Gly	Thr	Lys	Leu	Leu	Val	Leu	Asn	
		260						265					270			
Ser	Leu	Lys	Lys	Met	Met	Asn	Val	Ala	Glu	Leu	Glu	Leu	Gln	Asn	Cys	
		275					280					285				
Glu	Leu	Glu	Arg	Ile	Pro	His	Ala	Ile	Phe	Ser	Leu	Ser	Asn	Leu	Gln	
	290					295					300					
Glu	Leu	Asp	Leu	Lys	Ser	Asn	Asn	Ile	Arg	Thr	Ile	Glu	Glu	Ile	Ile	
305					310					315					320	
Ser	Phe	Gln	His	Leu	Lys	Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	His	Asn	
			325						330					335		
Lys	Ile	Val	Thr	Ile	Pro	Pro	Ser	Ile	Thr	His	Val	Lys	Asn	Leu	Glu	
			340					345					350			
Ser	Leu	Tyr	Phe	Ser	Asn	Asn	Lys	Leu	Glu	Ser	Leu	Pro	Val	Ala	Val	
		355					360					365				
Phe	Ser	Leu	Gln	Lys	Leu	Arg	Cys	Leu	Asp	Val	Ser	Tyr	Asn	Asn	Ile	
	370					375					380					

Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu
 385 390 395 400
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys
 405 410 415
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser
 420 425 430
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
 435 440 445
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
 450 455 460
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr
 465 470 475 480
 Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro
 485 490 495
 Phe Ala Asn Gly Ile
 500

<210> 186
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 186
 cctccctcta ttacccatgt c 21

<210> 187
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 187
 gaccaacttt ctctgggagt gagg 24

<210> 188
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 188

gtcactttat ttctctaaca acaagctcga atccttacca gtggcag

47

<210> 189

<211> 2917

<212> DNA

<213> Homo sapiens

<400> 189

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aagacatttg	tgttttacac	acataaggat	ctgtgttttg	ggtttcttct	tcctccccctg	180
acattggcat	tgcttagtg	ttgtgtgggg	agggagacca	cgtagggctca	gtgcttgctt	240
gcacttatct	gcctaggtac	atcgaagtct	tttgacctcc	atacagtgat	tatgcctgtc	300
atcgctgggtg	gtatcctggc	ggccttgctc	ctgctgatag	ttgtcgtgct	ctgtctttac	360
ttcaaaatac	acaacgcgct	aaaagctgca	aaggaacctg	aagctgtggc	tgtaaaaaat	420
cacaaccag	acaaggtgtg	gtgggccaa	aacagccagg	ccaaaacat	tgccacggag	480
tcttgtcctg	ccctgcagtg	ctgtgaagga	tatagaatgt	gtgccagttt	tgattccctg	540
ccaccttgct	gttgcgacat	aaatgagggc	ctctgagtta	ggaaaggctc	ccttctcaaa	600
gcagagccct	gaagacttca	atgatgtcaa	tgaggccacc	tgtttgat	gtgcaggcac	660
agaagaaagg	cacagctccc	catcagtttc	atggaaaata	actcagtgcc	tgctgggaac	720
cagctgctgg	agatccctac	agagagcttc	cactgggggc	aaccttcca	ggaaggagt	780
ggggagagag	aacctcact	gtggggaatg	ctgataaacc	agtcacacag	ctgctctatt	840
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gctgatgtaa	cacagagcct	ataaaagctg	tcggctctta	aggctgcca	gcgccttgcc	960
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tggacaatag	aaagaccaga	aaacaaaagc	atcagaatta	tcctttccta	tgtccagctt	1200
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gtccctctta	atggatgtgg	tacaatcaga	aaggtagaag	atcagtcaat	tacttacacc	1980
aatataatca	ccttttctgc	atcctcaact	tctgaagtga	tcacccgtca	gaaacaactc	2040
cagattattg	tgaagtgtga	aatgggacat	aattctacag	tggagataat	atacataaca	2100
gaagatgatg	taatacaaa	tcaaaatgca	ctgggcaa	ataacaccag	catggctctt	2160
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gttttgatat	gtgatagcag	tgaccaccag	tctcgtgca	atcaaggttg	tgtctccaga	2520
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ctgaaaagg	atcgaagtgc	aagtggcaat	tcaggatttc	agcatgaaac	acatgcggaa	2640
gaaactccaa	accagccttt	caacagtgtg	catctgtttt	ccttcatggg	tctagctctg	2700
aatgtggtga	ctgtagcgac	aatcacagt	aggcattttg	taaatcaacg	ggcagactac	2760
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 ggctgaaag tgacacacag gcctgcatgt aaaaaaa 2917

<210> 190
 <211> 607
 <212> PRT
 <213> Homo sapiens

<400> 190

Met	Glu	Leu	Val	Arg	Arg	Leu	Met	Pro	Leu	Thr	Leu	Leu	Ile	Leu	Ser	1	5	10	15
Cys	Leu	Ala	Glu	Leu	Thr	Met	Ala	Glu	Ala	Glu	Gly	Asn	Ala	Ser	Cys	20	25	30	
Thr	Val	Ser	Leu	Gly	Gly	Ala	Asn	Met	Ala	Glu	Thr	His	Lys	Ala	Met	35	40	45	
Ile	Leu	Gln	Leu	Asn	Pro	Ser	Glu	Asn	Cys	Thr	Trp	Thr	Ile	Glu	Arg	50	55	60	
Pro	Glu	Asn	Lys	Ser	Ile	Arg	Ile	Ile	Phe	Ser	Tyr	Val	Gln	Leu	Asp	65	70	75	80
Pro	Asp	Gly	Ser	Cys	Glu	Ser	Glu	Asn	Ile	Lys	Val	Phe	Asp	Gly	Thr	85	90	95	
Ser	Ser	Asn	Gly	Pro	Leu	Leu	Gly	Gln	Val	Cys	Ser	Lys	Asn	Asp	Tyr	100	105	110	
Val	Pro	Val	Phe	Glu	Ser	Ser	Ser	Ser	Thr	Leu	Thr	Phe	Gln	Ile	Val	115	120	125	
Thr	Asp	Ser	Ala	Arg	Ile	Gln	Arg	Thr	Val	Phe	Val	Phe	Tyr	Tyr	Phe	130	135	140	
Phe	Ser	Pro	Asn	Ile	Ser	Ile	Pro	Asn	Cys	Gly	Gly	Tyr	Leu	Asp	Thr	145	150	155	160
Leu	Glu	Gly	Ser	Phe	Thr	Ser	Pro	Asn	Tyr	Pro	Lys	Pro	His	Pro	Glu	165	170	175	
Leu	Ala	Tyr	Cys	Val	Trp	His	Ile	Gln	Val	Glu	Lys	Asp	Tyr	Lys	Ile	180	185	190	
Lys	Leu	Asn	Phe	Lys	Glu	Ile	Phe	Leu	Glu	Ile	Asp	Lys	Gln	Cys	Lys	195	200	205	
Phe	Asp	Phe	Leu	Ala	Ile	Tyr	Asp	Gly	Pro	Ser	Thr	Asn	Ser	Gly	Leu	210	215	220	
Ile	Gly	Gln	Val	Cys	Gly	Arg	Val	Thr	Pro	Thr	Phe	Glu	Ser	Ser	Ser	225	230	235	240
Asn	Ser	Leu	Thr	Val	Val	Leu	Ser	Thr	Asp	Tyr	Ala	Asn	Ser	Tyr	Arg	245	250	255	

Gly	Phe	Ser	Ala	Ser	Tyr	Thr	Ser	Ile	Tyr	Ala	Glu	Asn	Ile	Asn	Thr	260	265	270
Thr	Ser	Leu	Thr	Cys	Ser	Ser	Asp	Arg	Met	Arg	Val	Ile	Ile	Ser	Lys	275	280	285
Ser	Tyr	Leu	Glu	Ala	Phe	Asn	Ser	Asn	Gly	Asn	Asn	Leu	Gln	Leu	Lys	290	295	300
Asp	Pro	Thr	Cys	Arg	Pro	Lys	Leu	Ser	Asn	Val	Val	Glu	Phe	Ser	Val	305	310	315
Pro	Leu	Asn	Gly	Cys	Gly	Thr	Ile	Arg	Lys	Val	Glu	Asp	Gln	Ser	Ile	325	330	335
Thr	Tyr	Thr	Asn	Ile	Ile	Thr	Phe	Ser	Ala	Ser	Ser	Thr	Ser	Glu	Val	340	345	350
Ile	Thr	Arg	Gln	Lys	Gln	Leu	Gln	Ile	Ile	Val	Lys	Cys	Glu	Met	Gly	355	360	365
His	Asn	Ser	Thr	Val	Glu	Ile	Ile	Tyr	Ile	Thr	Glu	Asp	Asp	Val	Ile	370	375	380
Gln	Ser	Gln	Asn	Ala	Leu	Gly	Lys	Tyr	Asn	Thr	Ser	Met	Ala	Leu	Phe	385	390	395
Glu	Ser	Asn	Ser	Phe	Glu	Lys	Thr	Ile	Leu	Glu	Ser	Pro	Tyr	Tyr	Val	405	410	415
Asp	Leu	Asn	Gln	Thr	Leu	Phe	Val	Gln	Val	Ser	Leu	His	Thr	Ser	Asp	420	425	430
Pro	Asn	Leu	Val	Val	Phe	Leu	Asp	Thr	Cys	Arg	Ala	Ser	Pro	Thr	Ser	435	440	445
Asp	Phe	Ala	Ser	Pro	Thr	Tyr	Asp	Leu	Ile	Lys	Ser	Gly	Cys	Ser	Arg	450	455	460
Asp	Glu	Thr	Cys	Lys	Val	Tyr	Pro	Leu	Phe	Gly	His	Tyr	Gly	Arg	Phe	465	470	475
Gln	Phe	Asn	Ala	Phe	Lys	Phe	Leu	Arg	Ser	Met	Ser	Ser	Val	Tyr	Leu	485	490	495
Gln	Cys	Lys	Val	Leu	Ile	Cys	Asp	Ser	Ser	Asp	His	Gln	Ser	Arg	Cys	500	505	510
Asn	Gln	Gly	Cys	Val	Ser	Arg	Ser	Lys	Arg	Asp	Ile	Ser	Ser	Tyr	Lys	515	520	525
Trp	Lys	Thr	Asp	Ser	Ile	Ile	Gly	Pro	Ile	Arg	Leu	Lys	Arg	Asp	Arg	530	535	540
Ser	Ala	Ser	Gly	Asn	Ser	Gly	Phe	Gln	His	Glu	Thr	His	Ala	Glu	Glu	545	550	555

Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val
565 570 575

Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe
580 585 590

Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr
595 600 605

<210> 191

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 191

tctctattcc aaactgtggc g

21

<210> 192

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 192

tttgatgacg attcgaaggt gg

22

<210> 193

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 193

ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc

47

<210> 194

<211> 2362

<212> DNA

<213> Homo sapiens

<400> 194

gacggaagaa cagcgctccc gagggccgcg gagcctgcag agaggacagc cggcctgcgc 60
cgggacatgc ggccccagga gctccccagg ctgcggttcc cggtgctgct gttgctgttg 120
ctgctgctgc cgccgcccgc gtgccctgcc cacagcgcca cgcgcttcga cccacctgg 180
gagtccttgg acgcccgcga gctgcccgcg tggtttgacc aggccaagtt cggcatcttc 240
atccactggg gagtggtttc cgtgcccagc ttcggtagcg agtggttctg gtggatttg 300
caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattaccc tcctagtgttc 360

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aaatatgaag attttggacc actattttaca gcaaaatttt ttaatgccaa ccagtgggca 420
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tttaccttgt gggggtcaga atattcgtgg aactggaatg ccatagatga ggggcccaag 540
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aactatcagc ctgaggttct gtggtcggat ggtgacggag gagcaccgga tcaatactgg 780
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taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2280
ttataaaaaa aagtttttct ttcttcaatt ataaattaac ataagtgtac tgtaacttta 2340
caaacgtttt aattttttaa accttttttg ctcttttgta ataacactta gcttaaaaca 2362
taaactcatt gtgcaaatgt aa

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<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

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Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
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Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
    20                      25                      30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
    35                      40                      45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
    50                      55                      60

Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
    65                      70                      75                      80

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro

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85

90

95

Ser	Phe	Lys	Tyr	Glu	Asp	Phe	Gly	Pro	Leu	Phe	Thr	Ala	Lys	Phe	Phe			
			100					105					110					
Asn	Ala	Asn	Gln	Trp	Ala	Asp	Ile	Phe	Gln	Ala	Ser	Gly	Ala	Lys	Tyr			
		115					120					125						
Ile	Val	Leu	Thr	Ser	Lys	His	His	Glu	Gly	Phe	Thr	Leu	Trp	Gly	Ser			
	130					135					140							
Glu	Tyr	Ser	Trp	Asn	Trp	Asn	Ala	Ile	Asp	Glu	Gly	Pro	Lys	Arg	Asp			
145					150				155						160			
Ile	Val	Lys	Glu	Leu	Glu	Val	Ala	Ile	Arg	Asn	Arg	Thr	Asp	Leu	Arg			
				165					170					175				
Phe	Gly	Leu	Tyr	Tyr	Ser	Leu	Phe	Glu	Trp	Phe	His	Pro	Leu	Phe	Leu			
		180						185					190					
Glu	Asp	Glu	Ser	Ser	Ser	Phe	His	Lys	Arg	Gln	Phe	Pro	Val	Ser	Lys			
	195						200					205						
Thr	Leu	Pro	Glu	Leu	Tyr	Glu	Leu	Val	Asn	Asn	Tyr	Gln	Pro	Glu	Val			
	210					215					220							
Leu	Trp	Ser	Asp	Gly	Asp	Gly	Gly	Ala	Pro	Asp	Gln	Tyr	Trp	Asn	Ser			
225					230					235					240			
Thr	Gly	Phe	Leu	Ala	Trp	Leu	Tyr	Asn	Glu	Ser	Pro	Val	Arg	Gly	Thr			
			245						250					255				
Val	Val	Thr	Asn	Asp	Arg	Trp	Gly	Ala	Gly	Ser	Ile	Cys	Lys	His	Gly			
			260					265					270					
Gly	Phe	Tyr	Thr	Cys	Ser	Asp	Arg	Tyr	Asn	Pro	Gly	His	Leu	Leu	Pro			
	275						280					285						
His	Lys	Trp	Glu	Asn	Cys	Met	Thr	Ile	Asp	Lys	Leu	Ser	Trp	Gly	Tyr			
	290					295					300							
Arg	Arg	Glu	Ala	Gly	Ile	Ser	Asp	Tyr	Leu	Thr	Ile	Glu	Glu	Leu	Val			
305					310					315					320			
Lys	Gln	Leu	Val	Glu	Thr	Val	Ser	Cys	Gly	Gly	Asn	Leu	Leu	Met	Asn			
				325					330					335				
Ile	Gly	Pro	Thr	Leu	Asp	Gly	Thr	Ile	Ser	Val	Val	Phe	Glu	Glu	Arg			
			340					345					350					
Leu	Arg	Gln	Val	Gly	Ser	Trp	Leu	Lys	Val	Asn	Gly	Glu	Ala	Ile	Tyr			
		355					360					365						
Glu	Thr	Tyr	Thr	Trp	Arg	Ser	Gln	Asn	Asp	Thr	Val	Thr	Pro	Asp	Val			
	370					375					380							
Trp	Tyr	Thr	Ser	Lys	Pro	Lys	Glu	Lys	Leu	Val	Tyr	Ala	Ile	Phe	Leu			

385		390		395		400									
Lys	Trp	Pro	Thr	Ser	Gly	Gln	Leu	Phe	Leu	Gly	His	Pro	Lys	Ala	Ile
				405					410					415	
Leu	Gly	Ala	Thr	Glu	Val	Lys	Leu	Leu	Gly	His	Gly	Gln	Pro	Leu	Asn
			420					425					430		
Trp	Ile	Ser	Leu	Glu	Gln	Asn	Gly	Ile	Met	Val	Glu	Leu	Pro	Gln	Leu
		435					440					445			
Thr	Ile	His	Gln	Met	Pro	Cys	Lys	Trp	Gly	Trp	Ala	Leu	Ala	Leu	Thr
	450					455					460				

Asn Val Ile
465

<210> 196
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 196
tggtttgacc aggccaagtt cgg 23

<210> 197
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 197
ggattcatcc tcaaggaaga gcgg 24

<210> 198
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 198
aacttgagc atcagccact ctgc 24

<210> 199
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 199

ttccgtgccc agcttcggta gcgagtgggt ctggtgggtat tggca

45

<210> 200

<211> 2372

<212> DNA

<213> Homo sapiens

<400> 200

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caaatgtatc	actagccctc	ctttttccaa	caagaaggga	ctgagagatg	cagaaatatt	2340
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<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

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		20					25						30			
Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	Ile	Thr	Leu	Val	Ser	Lys	Lys	Ala	
		35					40					45				
Asn	Gln	Gln	Leu	Asn	Phe	Thr	Glu	Ala	Lys	Glu	Ala	Cys	Arg	Leu	Leu	
	50					55					60					
Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu	Thr	Ala	Leu	Lys	Ala	
65					70					75					80	
Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val	Gly	Asp	Gly	Phe	Val	Val	
				85				90						95		
Ile	Ser	Arg	Ile	Ser	Pro	Asn	Pro	Lys	Cys	Gly	Lys	Asn	Gly	Val	Gly	
		100						105					110			
Val	Leu	Ile	Trp	Lys	Val	Pro	Val	Ser	Arg	Gln	Phe	Ala	Ala	Tyr	Cys	
		115					120					125				
Tyr	Asn	Ser	Ser	Asp	Thr	Trp	Thr	Asn	Ser	Cys	Ile	Pro	Glu	Ile	Ile	
	130					135					140					
Thr	Thr	Lys	Asp	Pro	Ile	Phe	Asn	Thr	Gln	Thr	Ala	Thr	Gln	Thr	Thr	
145					150					155					160	
Glu	Phe	Ile	Val	Ser	Asp	Ser	Thr	Tyr	Ser	Val	Ala	Ser	Pro	Tyr	Ser	
				165					170					175		
Thr	Ile	Pro	Ala	Pro	Thr	Thr	Thr	Pro	Pro	Ala	Pro	Ala	Ser	Thr	Ser	
		180						185					190			
Ile	Pro	Arg	Arg	Lys	Lys	Leu	Ile	Cys	Val	Thr	Glu	Val	Phe	Met	Glu	
	195					200						205				
Thr	Ser	Thr	Met	Ser	Thr	Glu	Thr	Glu	Pro	Phe	Val	Glu	Asn	Lys	Ala	
	210					215					220					
Ala	Phe	Lys	Asn	Glu	Ala	Ala	Gly	Phe	Gly	Gly	Val	Pro	Thr	Ala	Leu	
225					230					235					240	
Leu	Val	Leu	Ala	Leu	Leu	Phe	Phe	Gly	Ala	Ala	Ala	Gly	Leu	Gly	Phe	
				245					250					255		
Cys	Tyr	Val	Lys	Arg	Tyr	Val	Lys	Ala	Phe	Pro	Phe	Thr	Asn	Lys	Asn	
		260						265						270		

Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
275 280 285

Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
290 295 300

Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
305 310 315 320

Glu Val

<210> 202
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 202
gagctttcca tccaggtgtc atgc 24

<210> 203
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 203
gtcagtgaca gtacctactc gg 22

<210> 204
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 204
tggagcagga ggagtagtag tagg 24

<210> 205
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 205
aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt 50

<210> 206
<211> 1620
<212> DNA
<213> Homo sapiens

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<221> modified_base
<222> (973)..(973)
<223> a, t, c or g

<220>
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<223> a, t, c or g

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<223> a, t, c or g

<220>
<221> modified_base
<222> (1003)..(1003)
<223> a, t, c or g

<400> 206
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acatactccc cacaccagtt tgatggcttt ccgtaataaa aagattggga tttccttttt 1620

<210> 207
<211> 296
<212> PRT
<213> Homo sapiens

<400> 207

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Leu	Ser	Arg	Trp	Leu	Ala	Gln	Pro	Tyr	Tyr	Leu	Leu	Ser	Ala	Leu	Leu
			20					25					30		
Ser	Ala	Ala	Phe	Leu	Leu	Val	Arg	Lys	Leu	Pro	Pro	Leu	Cys	His	Gly
		35					40					45			
Leu	Pro	Thr	Gln	Arg	Glu	Asp	Gly	Asn	Pro	Cys	Asp	Phe	Asp	Trp	Arg
	50					55					60				
Glu	Val	Glu	Ile	Leu	Met	Phe	Leu	Ser	Ala	Ile	Val	Met	Met	Lys	Asn
65					70					75					80
Arg	Arg	Ser	Ile	Thr	Val	Glu	Gln	His	Ile	Gly	Asn	Ile	Phe	Met	Phe
			85						90					95	
Ser	Lys	Val	Ala	Asn	Thr	Ile	Leu	Phe	Phe	Arg	Leu	Asp	Ile	Arg	Met
			100					105					110		
Gly	Leu	Leu	Tyr	Ile	Thr	Leu	Cys	Ile	Val	Phe	Leu	Met	Thr	Cys	Lys
	115						120					125			
Pro	Pro	Leu	Tyr	Met	Gly	Pro	Glu	Tyr	Ile	Lys	Tyr	Phe	Asn	Asp	Lys
	130					135					140				
Thr	Ile	Asp	Glu	Glu	Leu	Glu	Arg	Asp	Lys	Arg	Val	Thr	Trp	Ile	Val
145					150					155					160
Glu	Phe	Phe	Ala	Asn	Trp	Ser	Asn	Asp	Cys	Gln	Ser	Phe	Ala	Pro	Ile
			165						170					175	
Tyr	Ala	Asp	Leu	Ser	Leu	Lys	Tyr	Asn	Cys	Thr	Gly	Leu	Asn	Phe	Gly
			180					185					190		
Lys	Val	Asp	Val	Gly	Arg	Tyr	Thr	Asp	Val	Ser	Thr	Arg	Tyr	Lys	Val
		195					200					205			
Ser	Thr	Ser	Pro	Leu	Thr	Lys	Gln	Leu	Pro	Thr	Leu	Ile	Leu	Phe	Gln
	210					215					220				
Gly	Gly	Lys	Glu	Ala	Met	Arg	Arg	Pro	Gln	Ile	Asp	Lys	Lys	Gly	Arg
225					230					235					240
Ala	Val	Ser	Trp	Thr	Phe	Ser	Glu	Glu	Asn	Val	Ile	Arg	Glu	Phe	Asn
			245						250					255	
Leu	Asn	Glu	Leu	Tyr	Gln	Arg	Ala	Lys	Lys	Leu	Ser	Lys	Ala	Gly	Asp
		260						265						270	

Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser
275 280 285

Asp Gly Glu Asn Lys Lys Asp Lys
290 295

<210> 208
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 208
gcttgatat tcgcatgggc ctac 24

<210> 209
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 209
tggagacaat atccctgagg 20

<210> 210
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 210
aacagttggc cacagcatgg cagg 24

<210> 211
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 211
ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212
<211> 1985

<213> Homo sapiens

$\langle 400 \rangle$ 212

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cccattgtct	ctgctgcccc	gctcctacgg	actgcccttc	tacaacggct	tctactactc	180
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aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1980
aaaaaa						1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr
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Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
50 55 60

Ser	Val	Ile	Leu	Pro	Cys	Arg	Tyr	Arg	Tyr	Glu	Pro	Ala	Leu	Val	Ser	65	70	75	80
Pro	Arg	Arg	Val	Arg	Val	Lys	Trp	Trp	Lys	Leu	Ser	Glu	Asn	Gly	Ala	85	90	95	
Pro	Glu	Lys	Asp	Val	Leu	Val	Ala	Ile	Gly	Leu	Arg	His	Arg	Ser	Phe	100	105	110	
Gly	Asp	Tyr	Gln	Gly	Arg	Val	His	Leu	Arg	Gln	Asp	Lys	Glu	His	Asp	115	120	125	
Val	Ser	Leu	Glu	Ile	Gln	Asp	Leu	Arg	Leu	Glu	Asp	Tyr	Gly	Arg	Tyr	130	135	140	
Arg	Cys	Glu	Val	Ile	Asp	Gly	Leu	Glu	Asp	Glu	Ser	Gly	Leu	Val	Glu	145	150	155	160
Leu	Glu	Leu	Arg	Gly	Val	Val	Phe	Pro	Tyr	Gln	Ser	Pro	Asn	Gly	Arg	165	170	175	
Tyr	Gln	Phe	Asn	Phe	His	Glu	Gly	Gln	Gln	Val	Cys	Ala	Glu	Gln	Ala	180	185	190	
Ala	Val	Val	Ala	Ser	Phe	Glu	Gln	Leu	Phe	Arg	Ala	Trp	Glu	Glu	Gly	195	200	205	
Leu	Asp	Trp	Cys	Asn	Ala	Gly	Trp	Leu	Gln	Asp	Ala	Thr	Val	Gln	Tyr	210	215	220	
Pro	Ile	Met	Leu	Pro	Arg	Gln	Pro	Cys	Gly	Gly	Pro	Gly	Leu	Ala	Pro	225	230	235	240
Gly	Val	Arg	Ser	Tyr	Gly	Pro	Arg	His	Arg	Arg	Leu	His	Arg	Tyr	Asp	245	250	255	
Val	Phe	Cys	Phe	Ala	Thr	Ala	Leu	Lys	Gly	Arg	Val	Tyr	Tyr	Leu	Glu	260	265	270	
His	Pro	Glu	Lys	Leu	Thr	Leu	Thr	Glu	Ala	Arg	Glu	Ala	Cys	Gln	Glu	275	280	285	
Asp	Asp	Ala	Thr	Ile	Ala	Lys	Val	Gly	Gln	Leu	Phe	Ala	Ala	Trp	Lys	290	295	300	
Phe	His	Gly	Leu	Asp	Arg	Cys	Asp	Ala	Gly	Trp	Leu	Ala	Asp	Gly	Ser	305	310	315	320
Val	Arg	Tyr	Pro	Val	Val	His	Pro	His	Pro	Asn	Cys	Gly	Pro	Pro	Glu	325	330	335	
Pro	Gly	Val	Arg	Ser	Phe	Gly	Phe	Pro	Asp	Pro	Gln	Ser	Arg	Leu	Tyr	340	345	350	
Gly	Val	Tyr	Cys	Tyr	Arg	Gln	His									355	360		

<210> 214
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 214
tgcttcgcta ctgccctc 18

<210> 215
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 215
ttcccttgtg ggttgag 18

<210> 216
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 216
agggctggaa gccagttc 18

<210> 217
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 217
agccagtgcg gaaatgcg 18

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 218
tgtccaaagt acacacacct gagg 24

<210> 219
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 219
gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220
<211> 1503
<212> DNA
<213> Homo sapiens

<400> 220
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<210> 221
<211> 328
<212> PRT
<213> Homo sapiens

<400> 221
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Arg	Val	His	Gln	Ala	Ala	Pro	Leu	Ser	Asp	Ala	Pro	His	Asp	Asp	Ala	35	40	45
His	Gly	Asn	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu	Gly	Arg	Glu	Val	50	55	60
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Gly	Arg	Ile	Val	Asp	Arg	Met	Asp	Arg	Ala	Gly	Asp	Gly	Asp	Gly	Trp	85	90	95
Val	Ser	Leu	Ala	Glu	Leu	Arg	Ala	Trp	Ile	Ala	His	Thr	Gln	Gln	Arg	100	105	110
His	Ile	Arg	Asp	Ser	Val	Ser	Ala	Ala	Trp	Asp	Thr	Tyr	Asp	Thr	Asp	115	120	125
Arg	Asp	Gly	Arg	Val	Gly	Trp	Glu	Glu	Leu	Arg	Asn	Ala	Thr	Tyr	Gly	130	135	140
His	Tyr	Ala	Pro	Gly	Glu	Glu	Phe	His	Asp	Val	Glu	Asp	Ala	Glu	Thr	145	150	155
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His	Pro	Glu	Glu	Phe	Pro	His	Met	Arg	Asp	Ile	Val	Ile	Ala	Glu	Thr	195	200	205
Leu	Glu	Asp	Leu	Asp	Arg	Asn	Lys	Asp	Gly	Tyr	Val	Gln	Val	Glu	Glu	210	215	220
Tyr	Ile	Ala	Asp	Leu	Tyr	Ser	Ala	Glu	Pro	Gly	Glu	Glu	Glu	Pro	Ala	225	230	235
Trp	Val	Gln	Thr	Glu	Arg	Gln	Gln	Phe	Arg	Asp	Phe	Arg	Asp	Leu	Asn	245	250	255
Lys	Asp	Gly	His	Leu	Asp	Gly	Ser	Glu	Val	Gly	His	Trp	Val	Leu	Pro	260	265	270
Pro	Ala	Gln	Asp	Gln	Pro	Leu	Val	Glu	Ala	Asn	His	Leu	Leu	His	Glu	275	280	285
Ser	Asp	Thr	Asp	Lys	Asp	Gly	Arg	Leu	Ser	Lys	Ala	Glu	Ile	Leu	Gly	290	295	300
Asn	Trp	Asn	Met	Phe	Val	Gly	Ser	Gln	Ala	Thr	Asn	Tyr	Gly	Glu	Asp	305	310	315
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Leu Thr Arg His His Asp Glu Leu
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<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 222

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20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 223

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<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 225

ccccctgag cgacgctccc ccatgatgac gccacggga actt

44

<210> 226

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 226

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<210> 227

<211> 550

<212> PRT

<213> Homo sapiens

<400> 227

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Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile
      20              25              30

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```

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
  35              40              45

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Ile	Val	Tyr	Ala	Ser	Val	Ser	Ser	Ile	Cys	Gly	Ala	Ala	Val	His	Arg		
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Gly	Val	Ile	Ser	Asn	Ser	Gly	Gly	Pro	Val	Arg	Val	Tyr	Ser	Leu	Pro		
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Gly	Arg	Glu	Asn	Tyr	Ser	Ser	Val	Asp	Ala	Asn	Gly	Ile	Gln	Ser	Gln		
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Ala	Val	Cys	Arg	Asn	Asn	Gly	Phe	Phe	Ser	Tyr	His	Met	Pro	Asn	Trp		
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Phe	Gly	Thr	Thr	Lys	Tyr	Val	Lys	Pro	Leu	Val	Gln	Lys	Leu	Cys	Thr		
			340					345					350				

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
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 Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg
 370 375 380
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 385 390 395 400
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
 405 410 415
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
 420 425 430
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp
 435 440 445
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
 450 455 460
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
 465 470 475 480
 Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile
 485 490 495
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
 500 505 510
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
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<210> 228

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 228

tggtctcgca caccgatc

18

<210> 229

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 229

ctgctgtcca caggggag

18

<210> 230

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 230

ccttgaagca tactgctc

18

<210> 231

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 231

gagatagcaa tttccgcc

18

<210> 232

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 232

ttcctcaaga gggcagcc

18

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 233

cttggcacca atgtccgaga tttc

24

<210> 234

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 234

gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg

45

<210> 235

<211> 2586

<212> DNA

<213> Homo sapiens

<400> 235

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<210> 236
<211> 350
<212> PRT
<213> Homo sapiens

<400> 236
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Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80
Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
85 90 95
Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
100 105 110
Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
115 120 125
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
130 135 140
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
145 150 155 160
Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
165 170 175
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
180 185 190
Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
195 200 205
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
210 215 220
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225 230 235 240
Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
 260 265 270
 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
 275 280 285
 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
 290 295 300
 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
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 325 330 335
 Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile
 340 345 350

<210> 237
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 237
 ggagctgcac cccttgc 17

<210> 238
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 238
 ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg 49

<210> 239
 <211> 24
 <212> DNA
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<220>
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<210> 240
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<400> 240

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<400> 243

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<210> 244

<211> 3679

<212> DNA

<213> Homo Sapien

<400> 244

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<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser
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Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu
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Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu
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Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly
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Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe
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Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His
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Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His
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Asp	Ser	Arg	Trp	Phe	Glu	Met	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met	185	190	195
Ile	Gly	Gly	Asn	Lys	Val	Asp	Ala	Ile	Leu	Asp	Met	Asn	Phe	Arg	200	205	210
Pro	Leu	Ala	Asn	Leu	Arg	Ser	Leu	Val	Leu	Ala	Gly	Met	Asn	Leu	215	220	225
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Ala	Leu	Glu	Gln	Val	Pro	Gly	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	260	265	270
Asn	Pro	Leu	Gln	Arg	Val	Gly	Pro	Gly	Asp	Phe	Ala	Asn	Met	Leu	275	280	285
His	Leu	Lys	Glu	Leu	Gly	Leu	Asn	Asn	Met	Glu	Glu	Leu	Val	Ser	290	295	300
Ile	Asp	Lys	Phe	Ala	Leu	Val	Asn	Leu	Pro	Glu	Leu	Thr	Lys	Leu	305	310	315
Asp	Ile	Thr	Asn	Asn	Pro	Arg	Leu	Ser	Phe	Ile	His	Pro	Arg	Ala	320	325	330
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Leu	Gln	Glu	Val	Gly	Leu	His	Gly	Asn	Pro	Ile	Arg	Cys	Asp	Cys	365	370	375
Val	Ile	Arg	Trp	Ala	Asn	Ala	Thr	Gly	Thr	Arg	Val	Arg	Phe	Ile	380	385	390
Glu	Pro	Gln	Ser	Thr	Leu	Cys	Ala	Glu	Pro	Pro	Asp	Leu	Gln	Arg	395	400	405
Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys	410	415	420
Leu	Pro	Leu	Ile	Ser	Pro	Arg	Ser	Phe	Pro	Pro	Ser	Leu	Gln	Val	425	430	435

Ala	Ser	Gly	Glu	Ser	Met	Val	Leu	His	Cys	Arg	Ala	Leu	Ala	Glu	440	445	450
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Ser	Val	Val	Val	Gly	Arg	Ala	Leu	Leu	Gln	Pro	Gly	Arg	Asp	Glu	515	520	525
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Ala	Leu	Ala	Arg	Leu	Pro	Arg	Gly	Thr	His	Ser	Tyr	Asn	Ile	Thr	575	580	585
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Phe	Ala	Asp	Ala	His	Thr	Gln	Leu	Ala	Cys	Val	Trp	Ala	Arg	Thr	605	610	615
Lys	Glu	Ala	Thr	Ser	Cys	His	Arg	Ala	Leu	Gly	Asp	Arg	Pro	Gly	620	625	630
Leu	Ile	Ala	Ile	Leu	Ala	Leu	Ala	Val	Leu	Leu	Leu	Ala	Ala	Gly	635	640	645
Leu	Ala	Ala	His	Leu	Gly	Thr	Gly	Gln	Pro	Arg	Lys	Gly	Val	Gly	650	655	660
Gly	Arg	Arg	Pro	Leu	Pro	Pro	Ala	Trp	Ala	Phe	Trp	Gly	Trp	Ser	665	670	675
Ala	Pro	Ser	Val	Arg	Val	Val	Ser	Ala	Pro	Leu	Val	Leu	Pro	Trp	680	685	690
Asn	Pro	Gly	Arg	Lys	Leu	Pro	Arg	Ser	Ser	Glu	Gly	Glu	Thr	Leu	695	700	705
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<220>
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<400> 247
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<210> 248
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<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

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				20					25					30					
Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg					
				35					40					45					
Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe					
				50					55					60					
Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr					
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Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu					
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Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys					
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Asn	Asp	Phe	Ala	Phe	Met	Leu	His	Leu	Ile	Asp	Gln	Tyr	Asp	Pro					
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Leu	Tyr	Ser	Lys	Arg	Phe	Ala	Val	Phe	Leu	Ser	Glu	Val	Ser	Glu					
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Asn	Lys	Leu	Arg	Gln	Leu	Asn	Leu	Asn	Asn	Glu	Trp	Thr	Leu	Asp					
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Lys	Leu	Arg	Gln	Arg	Leu	Thr	Lys	Asn	Ala	Gln	Asp	Lys	Leu	Glu					
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Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Ile	Pro	Asp	Thr	Val	Phe	Asp					
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Leu	Val	Glu	Leu	Glu	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro	Asp	Val					
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Thr	Ile	Pro	Pro	Ser	Ile	Ala	Gln	Leu	Thr	Gly	Leu	Lys	Glu	Leu					
				200					205					210					
Trp	Leu	Tyr	His	Thr	Ala	Ala	Lys	Ile	Glu	Ala	Pro	Ala	Leu	Ala					
				215					220					225					

Phe	Leu	Arg	Glu	Asn	Leu	Arg	Ala	Leu	His	Ile	Lys	Phe	Thr	Asp	230	235	240
Ile	Lys	Glu	Ile	Pro	Leu	Trp	Ile	Tyr	Ser	Leu	Lys	Thr	Leu	Glu	245	250	255
Glu	Leu	His	Leu	Thr	Gly	Asn	Leu	Ser	Ala	Glu	Asn	Asn	Arg	Tyr	260	265	270
Ile	Val	Ile	Asp	Gly	Leu	Arg	Glu	Leu	Lys	Arg	Leu	Lys	Val	Leu	275	280	285
Arg	Leu	Lys	Ser	Asn	Leu	Ser	Lys	Leu	Pro	Gln	Val	Val	Thr	Asp	290	295	300
Val	Gly	Val	His	Leu	Gln	Lys	Leu	Ser	Ile	Asn	Asn	Glu	Gly	Thr	305	310	315
Lys	Leu	Ile	Val	Leu	Asn	Ser	Leu	Lys	Lys	Met	Ala	Asn	Leu	Thr	320	325	330
Glu	Leu	Glu	Leu	Ile	Arg	Cys	Asp	Leu	Glu	Arg	Ile	Pro	His	Ser	335	340	345
Ile	Phe	Ser	Leu	His	Asn	Leu	Gln	Glu	Ile	Asp	Leu	Lys	Asp	Asn	350	355	360
Asn	Leu	Lys	Thr	Ile	Glu	Glu	Ile	Ile	Ser	Phe	Gln	His	Leu	His	365	370	375
Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile	380	385	390
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu	395	400	405
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys	410	415	420
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe	425	430	435
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala	440	445	450
Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln	455	460	465
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln	470	475	480
Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile	485	490	495
Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly			

500	505	510
Glu Cys Pro Leu Leu Lys Arg Ser Gly	Leu Val Val Glu Glu Asp	
515	520	525
Leu Phe Asn Thr Leu Pro Pro Glu Val	Lys Glu Arg Leu Trp Arg	
530	535	540
Ala Asp Lys Glu Gln Ala		
545		

<210> 251
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 251
 caacaatgag ggcaccaagc 20

<210> 252
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 252
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<210> 253
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 253
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<210> 254
 <211> 1650
 <212> DNA
 <213> Homo Sapien

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 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150
 tgggattatg tgacgggtccg caaggatgcc tacatgttct ggtggctcta 200

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cagagccacc tagtttgtct ttgtcagcgc cacgtgagac acctacaacg 950
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ttattcctga ggatcaatcc tggggaggcc aggctaccaa cgtctttgtg 1050
aacatggagg aggacttcat gaagccagtc attagcattg tggacgagtt 1100
gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150
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tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350
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gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550
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taaaaaattg atttgttttg atcaaaataa aggatgataa tagatattaa 1650

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met	Glu	Leu	Ala	Leu	Arg	Arg	Ser	Pro	Val	Pro	Arg	Trp	Leu	Leu
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Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
			20						25					30

Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
			35						40					45

Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn
			50						55					60

Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln
			65						70					75

Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu
			80						85					90

Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp
			95						100					105

Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr
			110						115					120

Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu
			125						130					135

Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe
			140						145					150

Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser
			155						160					165

Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu
			170						175					180

Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly
			185						190					195

Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu
			200						205					210

Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys
			215						220					225

Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala
			230						235					240

Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys
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245	250	255
Ala Glu Met Ile	Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr	
260	265	270
Asn Ile Leu Thr	Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser	
275	280	285
Leu Glu Phe Thr	Gln Ser His Leu Val Cys Leu Cys Gln Arg His	
290	295	300
Val Arg His Leu	Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly	
305	310	315
Pro Ile Arg Lys	Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp	
320	325	330
Gly Gly Gln Ala	Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe	
335	340	345
Met Lys Pro Val	Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly	
350	355	360
Ile Asn Val Thr	Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp	
365	370	375
Thr Met Gly Gln	Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu	
380	385	390
Leu Pro Lys Phe	Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp	
395	400	405
Pro Lys Ser Leu	Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn	
410	415	420
Leu Ala Phe Tyr	Trp Ile Leu Lys Ala Gly His Met Val Pro Ser	
425	430	435
Asp Gln Gly Asp	Met Ala Leu Lys Met Met Arg Leu Val Thr Gln	
440	445	450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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tgctgctggc tcgggctgga ctcaggaagc cggagtcgca ggaggcggcg 100

ccgttatcag gaccatgcgg cgcacgggtc atcacgtcgc gcatcgtggg 150

tggagaggac gccgaactcg ggcgttgccc gtggcagggg agcctgcgcc 200

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tgtgggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctgggca 250
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cgggtgggatg gtccagtttg gccagctgac ttccatgcca tccttctgga 350
gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400
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tgcacctgtc acctacacta aacacatcca gcccatctgt ctccaggcct 500
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<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

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Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser

          20           25           30

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly
          35           40           45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
          50           55           60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
          65           70           75

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Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu	80	85	90
Ser	Asp	Pro	Ser	Gly	Trp	Met	Val	Gln	Phe	Gly	Gln	Leu	Thr	Ser	95	100	105
Met	Pro	Ser	Phe	Trp	Ser	Leu	Gln	Ala	Tyr	Tyr	Thr	Arg	Tyr	Phe	110	115	120
Val	Ser	Asn	Ile	Tyr	Leu	Ser	Pro	Arg	Tyr	Leu	Gly	Asn	Ser	Pro	125	130	135
Tyr	Asp	Ile	Ala	Leu	Val	Lys	Leu	Ser	Ala	Pro	Val	Thr	Tyr	Thr	140	145	150
Lys	His	Ile	Gln	Pro	Ile	Cys	Leu	Gln	Ala	Ser	Thr	Phe	Glu	Phe	155	160	165
Glu	Asn	Arg	Thr	Asp	Cys	Trp	Val	Thr	Gly	Trp	Gly	Tyr	Ile	Lys	170	175	180
Glu	Asp	Glu	Ala	Leu	Pro	Ser	Pro	His	Thr	Leu	Gln	Glu	Val	Gln	185	190	195
Val	Ala	Ile	Ile	Asn	Asn	Ser	Met	Cys	Asn	His	Leu	Phe	Leu	Lys	200	205	210
Tyr	Ser	Phe	Arg	Lys	Asp	Ile	Phe	Gly	Asp	Met	Val	Cys	Ala	Gly	215	220	225
Asn	Ala	Gln	Gly	Gly	Lys	Asp	Ala	Cys	Phe	Gly	Asp	Ser	Gly	Gly	230	235	240
Pro	Leu	Ala	Cys	Asn	Lys	Asn	Gly	Leu	Trp	Tyr	Gln	Ile	Gly	Val	245	250	255
Val	Ser	Trp	Gly	Val	Gly	Cys	Gly	Arg	Pro	Asn	Arg	Pro	Gly	Val	260	265	270
Tyr	Thr	Asn	Ile	Ser	His	His	Phe	Glu	Trp	Ile	Gln	Lys	Leu	Met	275	280	285
Ala	Gln	Ser	Gly	Met	Ser	Gln	Pro	Asp	Pro	Ser	Trp	Pro	Leu	Leu	290	295	300
Phe	Phe	Pro	Leu	Leu	Trp	Ala	Leu	Pro	Leu	Leu	Gly	Pro	Val		305	310	

<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

<400> 258

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cggagcccga ccagcggagg acgctgcccc caggctgggt gtccctgggc 150
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gaatgtggaa agactctcgg agctggtgca ggctgtgtcg gatcccagct 250
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aggccatccc cactgaccct ccacacggtg caaaaatggc tcttggcagc 350
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<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

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Ser	Gly	Lys	Cys	Ser	Tyr	Ser	Pro	Glu	Pro	Asp	Gln	Arg	Arg	Thr
				20				25					30	

Leu	Pro	Pro	Gly	Trp	Val	Ser	Leu	Gly	Arg	Ala	Asp	Pro	Glu	Glu
				35				40					45	

Glu	Leu	Ser	Leu	Thr	Phe	Ala	Leu	Arg	Gln	Gln	Asn	Val	Glu	Arg
				50				55					60	

Leu	Ser	Glu	Leu	Val	Gln	Ala	Val	Ser	Asp	Pro	Ser	Ser	Pro	Gln	65	70	75
Tyr	Gly	Lys	Tyr	Leu	Thr	Leu	Glu	Asn	Val	Ala	Asp	Leu	Val	Arg	80	85	90
Pro	Ser	Pro	Leu	Thr	Leu	His	Thr	Val	Gln	Lys	Trp	Leu	Leu	Ala	95	100	105
Ala	Gly	Ala	Gln	Lys	Cys	His	Ser	Val	Ile	Thr	Gln	Asp	Phe	Leu	110	115	120
Thr	Cys	Trp	Leu	Ser	Ile	Arg	Gln	Ala	Glu	Leu	Leu	Leu	Pro	Gly	125	130	135
Ala	Glu	Phe	His	His	Tyr	Val	Gly	Gly	Pro	Thr	Glu	Thr	His	Val	140	145	150
Val	Arg	Ser	Pro	His	Pro	Tyr	Gln	Leu	Pro	Gln	Ala	Leu	Ala	Pro	155	160	165
His	Val	Asp	Phe	Val	Gly	Gly	Leu	His	Arg	Phe	Pro	Pro	Thr	Ser	170	175	180
Ser	Leu	Arg	Gln	Arg	Pro	Glu	Pro	Gln	Val	Thr	Gly	Thr	Val	Gly	185	190	195
Leu	His	Leu	Gly	Val	Thr	Pro	Ser	Val	Ile	Arg	Lys	Arg	Tyr	Asn	200	205	210
Leu	Thr	Ser	Gln	Asp	Val	Gly	Ser	Gly	Thr	Ser	Asn	Asn	Ser	Gln	215	220	225
Ala	Cys	Ala	Gln	Phe	Leu	Glu	Gln	Tyr	Phe	His	Asp	Ser	Asp	Leu	230	235	240
Ala	Gln	Phe	Met	Arg	Leu	Phe	Gly	Gly	Asn	Phe	Ala	His	Gln	Ala	245	250	255
Ser	Val	Ala	Arg	Val	Val	Gly	Gln	Gln	Gly	Arg	Gly	Arg	Ala	Gly	260	265	270
Ile	Glu	Ala	Ser	Leu	Asp	Val	Gln	Tyr	Leu	Met	Ser	Ala	Gly	Ala	275	280	285
Asn	Ile	Ser	Thr	Trp	Val	Tyr	Ser	Ser	Pro	Gly	Arg	His	Glu	Gly	290	295	300
Gln	Glu	Pro	Phe	Leu	Gln	Trp	Leu	Met	Leu	Leu	Ser	Asn	Glu	Ser	305	310	315
Ala	Leu	Pro	His	Val	His	Thr	Val	Ser	Tyr	Gly	Asp	Asp	Glu	Asp	320	325	330
Ser	Leu	Ser	Ser	Ala	Tyr	Ile	Gln	Arg	Val	Asn	Thr	Glu	Leu	Met	335	340	345

Lys	Ala	Ala	Ala	Arg	Gly	Leu	Thr	Leu	Leu	Phe	Ala	Ser	Gly	Asp	350	355	360
Ser	Gly	Ala	Gly	Cys	Trp	Ser	Val	Ser	Gly	Arg	His	Gln	Phe	Arg	365	370	375
Pro	Thr	Phe	Pro	Ala	Ser	Ser	Pro	Tyr	Val	Thr	Thr	Val	Gly	Gly	380	385	390
Thr	Ser	Phe	Gln	Glu	Pro	Phe	Leu	Ile	Thr	Asn	Glu	Ile	Val	Asp	395	400	405
Tyr	Ile	Ser	Gly	Gly	Gly	Phe	Ser	Asn	Val	Phe	Pro	Arg	Pro	Ser	410	415	420
Tyr	Gln	Glu	Glu	Ala	Val	Thr	Lys	Phe	Leu	Ser	Ser	Ser	Pro	His	425	430	435
Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro	440	445	450
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg	455	460	465
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val	470	475	480
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser	485	490	495
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln	500	505	510
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser	515	520	525
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro	530	535	540
Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu	545	550	555

Cys

<210> 260

<211> 1638

<212> DNA

<213> Homo Sapien

<400> 260

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agtgagccct tacagtgcc cctggaaacc cacttggcct gcataccgcc 200

tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250
ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300
taagggaact cctactgcca cttacgaaga ggccaagcaa tatctgtctt 350
atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcatc 400
tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450
ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500
tcagcatttt tgggaaggac ttctgtctca actacccttt ctcaacatca 550
gtgaagtatt ccacgggctg caccggcacc ctgggtggcag agaagcatgt 600
cctcacagct gccactgca tacacgatgg aaaaacctat gtgaaaggaa 650
cccagaagct tcgagtgggc ttcttaaagc ccaagttaa agatggtggt 700
cgagggggcca acgactccac ttcagccatg cccgagcaga tgaaatttca 750
gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaagggca 800
atgccaatga catcggcag gattatgatt atgccctcct ggaactcaaa 850
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctcttgctaa 900
gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000
ttgctctacc agcaatgcga tgcccagcca ggggccagcg ggtctgggg 1050
ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaatta 1100
ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150
gatttcaacg tggctgtcag aatcactcct ctcaaatatg cccagatttg 1200
ctattggatt aaaggaaact acctggattg tagggagggg tgacacagt 1250
ttccctcctg gcagcaatta agggcttca tgttcttatt ttaggagagg 1300
ccaaattggt tttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350
tgtgtgtaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400
tgactggctt tactatttga aaactgggtt gtgtatcata tcatatatca 1450
tttaagcagt ttgaaggcat acttttgcag agaaataaaa aaaatactga 1500
tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550
caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600

atatttggca tacaagagat atgaaaaaaaa aaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu
1				5					10					15
Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
				20					25					30
Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr
				35					40					45
Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu
				50					55					60
Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
				65					70					75
Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu
				80					85					90
Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
				95					100					105
Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
				110					115					120
Ser	Gly	Lys	Ser	Arg	Arg	Lys	Arg	Gln	Ile	Tyr	Gly	Tyr	Asp	Ser
				125					130					135
Arg	Phe	Ser	Ile	Phe	Gly	Lys	Asp	Phe	Leu	Leu	Asn	Tyr	Pro	Phe
				140					145					150
Ser	Thr	Ser	Val	Lys	Leu	Ser	Thr	Gly	Cys	Thr	Gly	Thr	Leu	Val
				155					160					165
Ala	Glu	Lys	His	Val	Leu	Thr	Ala	Ala	His	Cys	Ile	His	Asp	Gly
				170					175					180
Lys	Thr	Tyr	Val	Lys	Gly	Thr	Gln	Lys	Leu	Arg	Val	Gly	Phe	Leu
				185					190					195
Lys	Pro	Lys	Phe	Lys	Asp	Gly	Gly	Arg	Gly	Ala	Asn	Asp	Ser	Thr
				200					205					210
Ser	Ala	Met	Pro	Glu	Gln	Met	Lys	Phe	Gln	Trp	Ile	Arg	Val	Lys
				215					220					225
Arg	Thr	His	Val	Pro	Lys	Gly	Trp	Ile	Lys	Gly	Asn	Ala	Asn	Asp
				230					235					240

Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro	245	250	255
His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys	260	265	270
Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp	275	280	285
Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu	290	295	300
Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala	305	310	315
Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln	320	325	330
Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp	335	340	345
Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg	350	355	360
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly	365	370	375
Asn Tyr Leu Asp Cys Arg Glu Gly	380		

<210> 262
 <211> 1378
 <212> DNA
 <213> Homo Sapien

<400> 262
 gcatcgccct gggctctctcg agcctgctgc ctgctcccc gccccaccag 50
 ccatgggtggt ttctggagcg cccccagccc tgggtggggg ctgtctcggc 100
 accttcacct ccctgctgct gctggcgctcg acagccatcc tcaatgcggc 150
 caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200
 ttgtgggagg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250
 atccagaaga atgggaccca cactgcgca ggttctctgc tcaccagccg 300
 ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaacct 350
 acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400
 cgggtcccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450
 ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctcgagcgct 500
 ccatacagtt ctgagagcgg gtcctgcca tctgcctacc tgatgcctct 550

atccacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600
 ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650
 ttcctatcat cgactcgga gtctgcagcc atctgtactg gcggggagca 700
 ggacagggac ccatcactga ggacatgctg tgtgccggct acttggaggg 750
 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800
 tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850
 gccgagcgca acaggcccg ggtctacatc agcctctctg cgcaccgctc 900
 ctgggtggag aagatcgtgc aaggggtgca gctccgctgg cgcgctcagg 950
 ggggtggggc cctcagggca ccgagccagg gctctggggc cgccgcgcgc 1000
 tcctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050
 cacatctgga tctggatctg cggcggcctc gggcggtttc ccccgccgta 1100
 aataggctca tctacctta cctctggggg cccggacggc tgctgcggaa 1150
 aggaaacccc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200
 catcaggccc cgcccaacgg cctcatgtcc ccgccccac gacttccggc 1250
 cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300
 ataggtattt gtaaccctgc ccacatatct tatttatcc tccaatttca 1350
 ataaattatt tattctccaa aaaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu
1				5					10					15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu
				20					25					30
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
				35					40					45
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu
				50					55					60
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
				65					70					75

Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180
Gly	Ser	Ile	Gln	Asp	Gly	Val	Pro	Leu	Pro	His	Pro	Gln	Thr	Leu	185	190	195
Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile	Asp	Ser	Glu	Val	Cys	Ser	His	200	205	210
Leu	Tyr	Trp	Arg	Gly	Ala	Gly	Gln	Gly	Pro	Ile	Thr	Glu	Asp	Met	215	220	225
Leu	Cys	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	Arg	Asp	Ala	Cys	Leu	Gly	230	235	240
Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Gln	Val	Asp	Gly	Ala	Trp	Leu	245	250	255
Leu	Ala	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Gly	Cys	Ala	Glu	Arg	Asn	260	265	270
Arg	Pro	Gly	Val	Tyr	Ile	Ser	Leu	Ser	Ala	His	Arg	Ser	Trp	Val	275	280	285
Glu	Lys	Ile	Val	Gln	Gly	Val	Gln	Leu	Arg	Gly	Arg	Ala	Gln	Gly	290	295	300
Gly	Gly	Ala	Leu	Arg	Ala	Pro	Ser	Gln	Gly	Ser	Gly	Ala	Ala	Ala	305	310	315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264
gtccgcaagg atgcctacat gttc 24

<210> 265
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 265
gcagaggtgt ctaaggttg 19

<210> 266
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 266
agctctagac caatgccagc ttcc 24

<210> 267
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 267
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 268
ggggaattca ccctatgaca ttgcc 25

<210> 269
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 269

gaatgccctg caagcatcaa ctgg 24

<210> 270

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 270

gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 271

gcggaagggc agaatgggac tccaag 26

<210> 272

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 272

cagccctgcc acatgtgc 18

<210> 273

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 273

tactgggtgg tcagcaac 18

<210> 274

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 274

ggcgaagagc agggtagagac cccg 24

<210> 275
<211> 45

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 275
gccctcatcc tctctggcaa atgcagttac agcccggagc cgcac 45

<210> 276
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 276
gggcagggat tccagggctc c 21

<210> 277
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 277
ggctatgaca gcaggttc 18

<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 278
tgacaatgac cgaccagg 18

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 279
gcatcgcatc gctggttagag caag 24

<210> 280

<211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 280
 ttacagtgcc ccctggaaac ccacttgGCC tgcataccgc ctccc 45

 <210> 281
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 281
 cgtctcgagc gtcataca gttcccttgc ccca 34

 <210> 282
 <211> 61
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 282
 tggaggggga gcgggatgct tgtctgggCG actccggggg cccctcatg 50

 tgccaggtgg a 61

 <210> 283
 <211> 119
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 283
 ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50

 gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

 atgctgtgtg cgggtact 119

 <210> 284
 <211> 1875
 <212> DNA
 <213> Homo Sapien

 <400> 284
 gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100
agatgaggag aaacgtttga tgggtggagct gcacaacctc taccggggccc 150
aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200
ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt gggggccaca 250
caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300
gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350
tacaacctca gcgcccacc ctgcagccca ggccagatgt gcggccacta 400
cacgcagggtg gtatgggcca agacagagag gatcggctgt ggttcccact 450
tctgtgagaa gctccaggtt gttgaggaga ccaacatcga attactggtg 500
tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550
ggggactccg tgctcccaat gtccctctgg ctaccactgc aagaactccc 600
tctgtgaacc catcggaagc ccggaagatg ctcaggattt gccttacctg 650
gtaactgagg ccccatcctt ccgggcgact gaagcatcag actctaggaa 700
aatgggtact ccttcttccc tagcaacggg gattccggct ttcttggtaa 750
cagaggtctc aggctccctg gcaaccaagg ctctgcctgc tgtggaaacc 800
caggccccaa cttccttagc aacgaaagac ccgccctcca tggcaacaga 850
ggctccacct tgcgtaacaa ctgagggtccc ttccattttg gcagctcaca 900
gcctgcctc cttggatgag gagccagtta cttccccaa atcgacccat 950
gttcctatcc caaaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000
ctctaggagc ccagagaact ctctggaccc caagatgtcc ctgacagggg 1050
caagggaact cctaccccat gcccaggagg aggctgaggc tgaggctgag 1100
ttgcctcctt ccagtgaggt cttggcctca gtttttccag cccaggacaa 1150
gccaggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200
agtccctgcc caatttcccc aatacctctg ccaccgctaa tgccacgggt 1250
gggctgccc tggctctgca gtcgtccttg ccagggtgcag agggccctga 1300
caagcctagc gttgtgtcag ggctgaactc gggccctggg catgtgtggg 1350
gccctctcct gggactactg ctectgcctc ctctggtgtt ggctggaatc 1400
ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtcctcctgt 1450
catcttcccc accctgtccc cagcccctaa acaagatact tcttggttaa 1500

ggccctccgg aagggaaagg ctacggggca tgtgcctcat cacaccatcc 1550
 atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1600
 ggactgcaca ccggggccac acctctcctg cccctccctc ctgagtcctg 1650
 ggggtgggag gatttgaggg agctcactgc ctacctggcc tggggctgtc 1700
 tgccacacaca gcatgtgcgc tctccctgag tgcctgtgta gctggggatg 1750
 gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800
 tgagtggggg aggcagggac gagggaagga aagtaactcc tgactctcca 1850
 ataaaaacct gtccaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu	1	5	10	15
Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp	20	25	30	
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala	35	40	45	
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp	50	55	60	
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val	65	70	75	
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe	80	85	90	
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu	95	100	105	
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys	110	115	120	
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	125	130	135	
Lys	Thr	Glu	Arg	Ile	Gly	Cys	Gly	Ser	His	Phe	Cys	Glu	Lys	Leu	140	145	150	
Gln	Gly	Val	Glu	Glu	Thr	Asn	Ile	Glu	Leu	Leu	Val	Cys	Asn	Tyr	155	160	165	
Glu	Pro	Pro	Gly	Asn	Val	Lys	Gly	Lys	Arg	Pro	Tyr	Gln	Glu	Gly				

170					175					180				
Thr	Pro	Cys	Ser	Gln	Cys	Pro	Ser	Gly	Tyr	His	Cys	Lys	Asn	Ser
				185					190					195
Leu	Cys	Glu	Pro	Ile	Gly	Ser	Pro	Glu	Asp	Ala	Gln	Asp	Leu	Pro
				200					205					210
Tyr	Leu	Val	Thr	Glu	Ala	Pro	Ser	Phe	Arg	Ala	Thr	Glu	Ala	Ser
				215					220					225
Asp	Ser	Arg	Lys	Met	Gly	Thr	Pro	Ser	Ser	Leu	Ala	Thr	Gly	Ile
				230					235					240
Pro	Ala	Phe	Leu	Val	Thr	Glu	Val	Ser	Gly	Ser	Leu	Ala	Thr	Lys
				245					250					255
Ala	Leu	Pro	Ala	Val	Glu	Thr	Gln	Ala	Pro	Thr	Ser	Leu	Ala	Thr
				260					265					270
Lys	Asp	Pro	Pro	Ser	Met	Ala	Thr	Glu	Ala	Pro	Pro	Cys	Val	Thr
				275					280					285
Thr	Glu	Val	Pro	Ser	Ile	Leu	Ala	Ala	His	Ser	Leu	Pro	Ser	Leu
				290					295					300
Asp	Glu	Glu	Pro	Val	Thr	Phe	Pro	Lys	Ser	Thr	His	Val	Pro	Ile
				305					310					315
Pro	Lys	Ser	Ala	Asp	Lys	Val	Thr	Asp	Lys	Thr	Lys	Val	Pro	Ser
				320					325					330
Arg	Ser	Pro	Glu	Asn	Ser	Leu	Asp	Pro	Lys	Met	Ser	Leu	Thr	Gly
				335					340					345
Ala	Arg	Glu	Leu	Leu	Pro	His	Ala	Gln	Glu	Glu	Ala	Glu	Ala	Glu
				350					355					360
Ala	Glu	Leu	Pro	Pro	Ser	Ser	Glu	Val	Leu	Ala	Ser	Val	Phe	Pro
				365					370					375
Ala	Gln	Asp	Lys	Pro	Gly	Glu	Leu	Gln	Ala	Thr	Leu	Asp	His	Thr
				380					385					390
Gly	His	Thr	Ser	Ser	Lys	Ser	Leu	Pro	Asn	Phe	Pro	Asn	Thr	Ser
				395					400					405
Ala	Thr	Ala	Asn	Ala	Thr	Gly	Gly	Arg	Ala	Leu	Ala	Leu	Gln	Ser
				410					415					420
Ser	Leu	Pro	Gly	Ala	Glu	Gly	Pro	Asp	Lys	Pro	Ser	Val	Val	Ser
				425					430					435
Gly	Leu	Asn	Ser	Gly	Pro	Gly	His	Val	Trp	Gly	Pro	Leu	Leu	Gly
				440					445					450
Leu	Leu	Leu	Leu	Pro	Pro	Leu	Val	Leu	Ala	Gly	Ile	Phe		

<210> 286
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 286
tcctgcagtt tcctgatgc 19

<210> 287
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 287
ctcatattgc acaccagtaa ttcg 24

<210> 288
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 288
atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289
<211> 3662
<212> DNA
<213> Homo Sapien

<400> 289
gtaactgaag tcaggctttt catttgggaa gccccctcaa cagaattcgg 50
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 Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
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 Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn
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<212> DNA

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 Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser
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 Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe
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 Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg
 125 130 135
 Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu
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Gly	Thr	Val	Met	Thr	His	Gly	Ala	Tyr	Lys	Val	Arg	Ile	Ala	Val	395	400	405
Leu	Ser	Asp	Gly	Thr	Leu	Asn	Phe	Thr	Asn	Val	Thr	Val	Gln	Asp	410	415	420
Thr	Gly	Met	Tyr	Thr	Cys	Met	Val	Ser	Asn	Ser	Val	Gly	Asn	Thr	425	430	435

Thr	Ala	Ser	Ala	Thr	Leu	Asn	Val	Thr	Ala	Ala	Thr	Thr	Thr	Pro
					440				445					450
Phe	Ser	Tyr	Phe	Ser	Thr	Val	Thr	Val	Glu	Thr	Met	Glu	Pro	Ser
					455				460					465
Gln	Asp	Glu	Ala	Arg	Thr	Thr	Asp	Asn	Asn	Val	Gly	Pro	Thr	Pro
					470				475					480
Val	Val	Asp	Trp	Glu	Thr	Thr	Asn	Val	Thr	Thr	Ser	Leu	Thr	Pro
					485				490					495
Gln	Ser	Thr	Arg	Ser	Thr	Glu	Lys	Thr	Phe	Thr	Ile	Pro	Val	Thr
					500				505					510
Asp	Ile	Asn	Ser	Gly	Ile	Pro	Gly	Ile	Asp	Glu	Val	Met	Lys	Thr
					515				520					525
Thr	Lys	Ile	Ile	Ile	Gly	Cys	Phe	Val	Ala	Ile	Thr	Leu	Met	Ala
					530				535					540
Ala	Val	Met	Leu	Val	Ile	Phe	Tyr	Lys	Met	Arg	Lys	Gln	His	His
					545				550					555
Arg	Gln	Asn	His	His	Ala	Pro	Thr	Arg	Thr	Val	Glu	Ile	Ile	Asn
					560				565					570
Val	Asp	Asp	Glu	Ile	Thr	Gly	Asp	Thr	Pro	Met	Glu	Ser	His	Leu
					575				580					585
Pro	Met	Pro	Ala	Ile	Glu	His	Glu	His	Leu	Asn	His	Tyr	Asn	Ser
					590				595					600
Tyr	Lys	Ser	Pro	Phe	Asn	His	Thr	Thr	Thr	Val	Asn	Thr	Ile	Asn
					605				610					615
Ser	Ile	His	Ser	Ser	Val	His	Glu	Pro	Leu	Leu	Ile	Arg	Met	Asn
					620				625					630
Ser	Lys	Asp	Asn	Val	Gln	Glu	Thr	Gln	Ile					
					635				640					

<210> 293

<211> 4053

<212> DNA

<213> Homo Sapien

<400> 293

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gagggcgggc gtgcaccctc ggctggaagt ttgtgccggg ccccgagcgc 200

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attatctttc atcaaggcaa gttccatgag ccaccttcaa agccttcgag 550
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aaa 4053

<210> 294

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

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Leu	Leu	Cys	Ala	Val	Leu	Gly	Arg	Ala	Gly	Arg	Ser	Asp	Ser	Gly
				20				25					30	
Gly	Arg	Gly	Glu	Leu	Gly	Gln	Pro	Ser	Gly	Val	Ala	Ala	Glu	Arg
				35				40					45	

Pro	Cys	Pro	Thr	Thr	Cys	Arg	Cys	Leu	Gly	Asp	Leu	Leu	Asp	Cys		50	55	60
Ser	Arg	Lys	Arg	Leu	Ala	Arg	Leu	Pro	Glu	Pro	Leu	Pro	Ser	Trp		65	70	75
Val	Ala	Arg	Leu	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys		80	85	90
Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu		95	100	105
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser		110	115	120
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu		125	130	135
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu		140	145	150
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro		155	160	165
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr		170	175	180
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu		185	190	195
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys		200	205	210
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn		215	220	225
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala		230	235	240
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met		245	250	255
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu		260	265	270
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly		275	280	285
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn		290	295	300
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu		305	310	315
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser		320	325	330

Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	
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Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser	
				350					355					360	
Leu	Lys	Thr	Leu	Asp	Leu	Lys	Asn	Asn	Glu	Ile	Ser	Trp	Thr	Ile	
				365					370					375	
Glu	Asp	Met	Asn	Gly	Ala	Phe	Ser	Gly	Leu	Asp	Lys	Leu	Arg	Arg	
				380					385					390	
Leu	Ile	Leu	Gln	Gly	Asn	Arg	Ile	Arg	Ser	Ile	Thr	Lys	Lys	Ala	
				395					400					405	
Phe	Thr	Gly	Leu	Asp	Ala	Leu	Glu	His	Leu	Asp	Leu	Ser	Asp	Asn	
				410					415					420	
Ala	Ile	Met	Ser	Leu	Gln	Gly	Asn	Ala	Phe	Ser	Gln	Met	Lys	Lys	
				425					430					435	
Leu	Gln	Gln	Leu	His	Leu	Asn	Thr	Ser	Ser	Leu	Leu	Cys	Asp	Cys	
				440					445					450	
Gln	Leu	Lys	Trp	Leu	Pro	Gln	Trp	Val	Ala	Glu	Asn	Asn	Phe	Gln	
				455					460					465	
Ser	Phe	Val	Asn	Ala	Ser	Cys	Ala	His	Pro	Gln	Leu	Leu	Lys	Gly	
				470					475					480	
Arg	Ser	Ile	Phe	Ala	Val	Ser	Pro	Asp	Gly	Phe	Val	Cys	Asp	Asp	
				485					490					495	
Phe	Pro	Lys	Pro	Gln	Ile	Thr	Val	Gln	Pro	Glu	Thr	Gln	Ser	Ala	
				500					505					510	
Ile	Lys	Gly	Ser	Asn	Leu	Ser	Phe	Ile	Cys	Ser	Ala	Ala	Ser	Ser	
				515					520					525	
Ser	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu	
				530					535					540	
Leu	His	Asp	Ala	Glu	Met	Glu	Asn	Tyr	Ala	His	Leu	Arg	Ala	Gln	
				545					550					555	
Gly	Gly	Glu	Val	Met	Glu	Tyr	Thr	Thr	Ile	Leu	Arg	Leu	Arg	Glu	
				560					565					570	
Val	Glu	Phe	Ala	Ser	Glu	Gly	Lys	Tyr	Gln	Cys	Val	Ile	Ser	Asn	
				575					580					585	
His	Phe	Gly	Ser	Ser	Tyr	Ser	Val	Lys	Ala	Lys	Leu	Thr	Val	Asn	
				590					595					600	
Met	Leu	Pro	Ser	Phe	Thr	Lys	Thr	Pro	Met	Asp	Leu	Thr	Ile	Arg	
				605					610					615	

Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His	Pro
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Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe	Pro
635		640	645
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val
650		655	660
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser
665		670	675
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr
680		685	690
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp
695		700	705
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala
710		715	720
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser
725		730	735
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln
740		745	750
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr
755		760	765
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val
770		775	780
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met
785		790	795
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val
800		805	810
Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu	Val
815		820	825
Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp	Cys
830		835	840
Ser Ile Thr Asn	Thr Asp Glu Thr Asn	Leu Pro Ala Asp Ile	Pro
845		850	855
Ser Tyr Leu Ser	Ser Gln Gly Thr Leu	Ala Asp Arg Gln Asp	Gly
860		865	870
Tyr Val Ser Ser	Glu Ser Gly Ser His	His Gln Phe Val Thr	Ser
875		880	885
Ser Gly Ala Gly	Phe Phe Leu Pro Gln	His Asp Ser Ser Gly	Thr
890		895	900

Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr	905	910	915
Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr	920	925	930
Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His	935	940	945
Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr	950	955	960
Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His	965	970	975
Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp	980	985	990
Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn	995	1000	1005
Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu	1010	1015	1020
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn	1025	1030	1035
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu	1040	1045	1050
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg	1055	1060	1065
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly	1070	1075	1080
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn	1085	1090	1095
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro	1100	1105	1110
Asn Phe Gln Ser Tyr Asp Leu Asp Thr	1115		

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<211> 18

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<223> Synthetic Oligonucleotide Probe

<400> 295

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<212> DNA
<213> Artificial Sequence

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<400> 296
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<210> 297
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 297
ggctggagac actgaacct 19

<210> 298
<211> 24
<212> DNA
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<400> 298
acagctgcac agctcagaac agtg 24

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<210> 300
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<212> DNA
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<400> 300
gggtcttggt gaatgagg 18

<210> 301

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<400> 305
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<210> 306
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<212> DNA
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<400> 306
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<210> 308
<211> 24
<212> DNA
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<223> Synthetic Oligonucleotide Probe

<400> 308
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<210> 309
<211> 50
<212> DNA
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<220>
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<210> 310
<211> 3296
<212> DNA
<213> Homo Sapien

<400> 310

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<210> 311
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 311
gcattggccg cgagactttg cc 22

<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 312
gcggccacgg tccttggaat tg 22

<210> 313
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 313
tggaggagct caacctcagc tacaaccgca tcaccagccc acagg 45

<210> 314
<211> 3003
<212> DNA
<213> Homo Sapien

<400> 314
gggagggggc tccgggagc ggcagcaga cctgctcgg ccgagcgcct 50
cgccgctgtc ctccgggagc ggcagcagta gcccgggcgg cgagggctgg 100
gggttcctcg agactctcag aggggcgcct cccatcggcg cccaccacc 150
caacctgttc ctgcgcgcgc actgcgctgc gcccaggac ccgctgcca 200

acatggattt tctcctggcg ctggtgctgg tatectcgct ctacctgcag 250
gcggccgcgc agttcgacgg gaggtggccc aggcaaatag tgtcatcgat 300
tggcctatgt cgttatgggtg ggaggattga ctgctgctgg ggctgggctc 350
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aat 3003

<210> 315
 <211> 509
 <212> PRT
 <213> Homo Sapien

<400> 315
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 1 5 10 15
 Gln Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro Arg Gln Ile Val
 20 25 30
 Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys
 35 40 45
 Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
 50 55 60
 Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
 65 70 75
 Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu
 80 85 90
 Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met
 95 100 105
 Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met
 110 115 120
 Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met
 125 130 135
 Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg
 140 145 150
 Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg
 155 160 165
 Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys
 170 175 180
 Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys
 185 190 195
 Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr
 200 205 210
 Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys
 215 220 225
 Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys
 230 235 240
 Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr
 245 250 255

Ile	Pro	Lys	Val	Met	Ile	Glu	Pro	Ser	Gly	Pro	Ile	His	Val	Pro	260	265	270
Lys	Gly	Asn	Gly	Thr	Ile	Leu	Lys	Gly	Asp	Thr	Gly	Asn	Asn	Asn	275	280	285
Trp	Ile	Pro	Asp	Val	Gly	Ser	Thr	Trp	Trp	Pro	Pro	Lys	Thr	Pro	290	295	300
Tyr	Ile	Pro	Pro	Ile	Ile	Thr	Asn	Arg	Pro	Thr	Ser	Lys	Pro	Thr	305	310	315
Thr	Arg	Pro	Thr	Pro	Lys	Pro	Thr	Pro	Ile	Pro	Thr	Pro	Pro	Pro	320	325	330
Pro	Pro	Pro	Leu	Pro	Thr	Glu	Leu	Arg	Thr	Pro	Leu	Pro	Pro	Thr	335	340	345
Thr	Pro	Glu	Arg	Pro	Thr	Thr	Gly	Leu	Thr	Thr	Ile	Ala	Pro	Ala	350	355	360
Ala	Ser	Thr	Pro	Pro	Gly	Gly	Ile	Thr	Val	Asp	Asn	Arg	Val	Gln	365	370	375
Thr	Asp	Pro	Gln	Lys	Pro	Arg	Gly	Asp	Val	Phe	Ser	Val	Leu	Val	380	385	390
His	Ser	Cys	Asn	Phe	Asp	His	Gly	Leu	Cys	Gly	Trp	Ile	Arg	Glu	395	400	405
Lys	Asp	Asn	Asp	Leu	His	Trp	Glu	Pro	Ile	Arg	Asp	Pro	Ala	Gly	410	415	420
Gly	Gln	Tyr	Leu	Thr	Val	Ser	Ala	Ala	Lys	Ala	Pro	Gly	Gly	Lys	425	430	435
Ala	Ala	Arg	Leu	Val	Leu	Pro	Leu	Gly	Arg	Leu	Met	His	Ser	Gly	440	445	450
Asp	Leu	Cys	Leu	Ser	Phe	Arg	His	Lys	Val	Thr	Gly	Leu	His	Ser	455	460	465
Gly	Thr	Leu	Gln	Val	Phe	Val	Arg	Lys	His	Gly	Ala	His	Gly	Ala	470	475	480
Ala	Leu	Trp	Gly	Arg	Asn	Gly	Gly	His	Gly	Trp	Arg	Gln	Thr	Gln	485	490	495
Ile	Thr	Leu	Arg	Gly	Ala	Asp	Ile	Lys	Ser	Glu	Ser	Gln	Arg		500	505	

<210> 316

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 316

gatggttcct gctcaagtgc cctg 24

<210> 317

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 317

ttgcacttgt aggaccacg tacg 24

<210> 318

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 318

ctgatgggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

<210> 319

<211> 2110

<212> DNA

<213> Homo Sapien

<400> 319

cttctttgaa aaggattatc acctgatcag gttctctctg catttgcccc 50

tttagattgt gaaatgtggc tcaagggtctt cacaactttc ctttcctttg 100

caacagggtgc ttgctcgggg ctgaagggtga cagtgccatc acacactgtc 150

catggcgctca gaggtcaggc cctctaccta cccgtccact atggcttcca 200

cactccagca tcagacatcc agatcatatg gctatttgag agacccaca 250

caatgcccaa atacttactg ggctctgtga ataagtctgt ggcttcctgac 300

ttggaatacc aacacaagtt caccatgatg ccaccaatg catctctgct 350

tatcaacca ctgcagttcc ctgatgaagg caattacatc gtgaagggtca 400

acattcaggg aaatggaact ctatctgcca gtcagaagat acaagtcacg 450

gttgatgatc ctgtcacaaa gccagtggtg cagattcatc ctccctctgg 500

ggctgtggag tatgtgggga acatgaccct gacatgcat gtggaagggg 550

gcactcggct agcttaccaa tggctaaaaa atgggagacc tgtccacacc 600
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acaaaactat gcctthctct ththththcaat caccagtagt atththtgaga 2000

agacttgtga acacttaagg aaatgactat taaagtctta tttttatttt 2050
 tttcaaggaa agatggattc aaataaatta ttctgttttt gcttttaaaa 2100
 aaaaaaaaaa 2110

<210> 320
 <211> 450
 <212> PRT
 <213> Homo Sapien

<400> 320
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 Ala Cys Ser Gly Leu Lys Val Thr Val Pro Ser His Thr Val His
 20 25 30
 Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe
 35 40 45
 His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg
 50 55 60
 Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser
 65 70 75
 Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro
 80 85 90
 Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu
 95 100 105
 Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu
 110 115 120
 Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr
 125 130 135
 Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr
 140 145 150
 Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg
 155 160 165
 Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser
 170 175 180
 Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala
 185 190 195
 Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg
 200 205 210
 Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile
 215 220 225

Tyr	Tyr	Gly	Pro	Tyr	Gly	Leu	Gln	Val	Asn	Ser	Asp	Lys	Gly	Leu	230	235	240
Lys	Val	Gly	Glu	Val	Phe	Thr	Val	Asp	Leu	Gly	Glu	Ala	Ile	Leu	245	250	255
Phe	Asp	Cys	Ser	Ala	Asp	Ser	His	Pro	Pro	Asn	Thr	Tyr	Ser	Trp	260	265	270
Ile	Arg	Arg	Thr	Asp	Asn	Thr	Thr	Tyr	Ile	Ile	Lys	His	Gly	Pro	275	280	285
Arg	Leu	Glu	Val	Ala	Ser	Glu	Lys	Val	Ala	Gln	Lys	Thr	Met	Asp	290	295	300
Tyr	Val	Cys	Cys	Ala	Tyr	Asn	Asn	Ile	Thr	Gly	Arg	Gln	Asp	Glu	305	310	315
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu	320	325	330
Ala	Gln	Lys	Gly	Lys	Ser	Leu	Ser	Pro	Leu	Ala	Ser	Ile	Thr	Gly	335	340	345
Ile	Ser	Leu	Phe	Leu	Ile	Ile	Ser	Met	Cys	Leu	Leu	Phe	Leu	Trp	350	355	360
Lys	Lys	Tyr	Gln	Pro	Tyr	Lys	Val	Ile	Lys	Gln	Lys	Leu	Glu	Gly	365	370	375
Arg	Pro	Glu	Thr	Glu	Tyr	Arg	Lys	Ala	Gln	Thr	Phe	Ser	Gly	His	380	385	390
Glu	Asp	Ala	Leu	Asp	Asp	Phe	Gly	Ile	Tyr	Glu	Phe	Val	Ala	Phe	395	400	405
Pro	Asp	Val	Ser	Gly	Val	Ser	Arg	Ile	Pro	Ser	Arg	Ser	Val	Pro	410	415	420
Ala	Ser	Asp	Cys	Val	Ser	Gly	Gln	Asp	Leu	His	Ser	Thr	Val	Tyr	425	430	435
Glu	Val	Ile	Gln	His	Ile	Pro	Ala	Gln	Gln	Gln	Asp	His	Pro	Glu	440	445	450

<210> 321

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 321

gatcctgtca caaagccagt ggtgc 25

<210> 322

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 322

cactgacagg gttcctcacc cagg 24

<210> 323

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

gcaagcggcg aaatggcgcc ctccgggagt cttgcagttc ccctggcagt 50

cctggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100

acgttcgct catcacggac gagaactgga gagaactgct ggaaggagac 150

tggatgatag aattttatgc cccgtggtgc cctgcttgtc aaaatcttca 200

accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250

ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggtttatc 300

ataactgctc ttctactat ttatcattgt aaagatgggt aatttaggcg 350

ctatcagggt ccaaggacta agaaggactt cataaaacttt ataagtata 400

aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450

gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500

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ctctgtatga tatttgtggc agattgcctt tgtccttcaa aaaggcgcag 650

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gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850
cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900
aagattgatc attttgtttg gtttgaagtg aactgtgact tttttgaata 950
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attttctctt gtatttttct tacttactat gggttacatt ttttattttt 1550
caaattggat gataatttct tggaaacatt ttttatgttt tagtaaacag 1600
tatttttttg ttgtttcaaa ctgaagttaa ctgagagatc catcaaattg 1650
aacaatctgt tgtaatttaa aattttggtc acttttttca gattttacat 1700
cattcttgct gaacttcaac ttgaaattgt tttttttttc tttttggatg 1750
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caggaaaaag catcttcttg tatatgtctt aaatgtattt ttgtcctcat 1900
atacagaaaag ttcttaattg attttacagt ctgtaatgct tgatgtttta 1950
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atagttttca ccttaaaaga agggggaaaa tcataaatac aatgaatcaa 2150

ctgaccatta cgtagtagac aatttctgta atgtcccctt ctttctaggc 2200
tctgttgctg tgtgaatcca ttagatttac agtatcgtaa tatacaagtt 2250
ttcttttaaag ccctctcctt tagaatttaa aatattgtac cattaaagag 2300
tttgatgtg taacttgtga tgccttagaa aaatataccta agcacaaaat 2350
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<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

Met	Ala	Pro	Ser	Gly	Ser	Leu	Ala	Val	Pro	Leu	Ala	Val	Leu	Val	1	5	10	15
Leu	Leu	Leu	Trp	Gly	Ala	Pro	Trp	Thr	His	Gly	Arg	Arg	Ser	Asn	20	25	30	
Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly	35	40	45	
Asp	Trp	Met	Ile	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Pro	Ala	Cys	Gln	50	55	60	
Asn	Leu	Gln	Pro	Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp	65	70	75	
Leu	Glu	Val	Asn	Ile	Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly	80	85	90	
Leu	Ser	Gly	Arg	Phe	Ile	Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His	95	100	105	
Cys	Lys	Asp	Gly	Glu	Phe	Arg	Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys	110	115	120	
Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	Asp	Lys	Glu	Trp	Lys	Ser	Ile	125	130	135	
Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	Gly	Ser	Val	Leu	Met	Ser	140	145	150	
Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	Trp	Ile	Arg	Thr	Cys	155	160	165	
His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	Val	Trp	Gly	Ser	170	175	180	
Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly	Leu	Leu	Leu	185	190	195	

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu
215 220 225

Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu
230 235 240

Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu
245 250 255

Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser
260 265 270

Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser
275 280

<210> 326

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 326

tgaggtgggc aagcggcgaa atg 23

<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 327

tatgtggatc aggacgtgcc 20

<210> 328

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 328

tgcagggttc agtctagatt g 21

<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 329

ttgaaggaca aaggcaatct gccac 25

<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

ggagtcttgc agttcccctg gcagtcctgg tgctgttgct ttggg 45

<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

gcgagtgtcc agctgcggag acccgtgata attcgттаac taattcaaca 50

aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccagtg 100

ggacaggcgg attggaagag cgggaaggtc ctggcccaga gcagtgtgac 150

acttccctct gtgacatga aactctgggt gtctgcattg ctgatggcct 200

ggtttgggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250

cacatgactg acctgattta tgcagagaaa gagctgggtgc agtctctgaa 300

agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350

ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400

tacctggctc accctgtgaa tgcctacaaa ctgggtgaagc ggctaaacac 450

agactggcct gcgctggagg accttgtcct gcaggactca gctgcagggtt 500

ttatcgccaa cctctctgtg cagcggcagt tcttccccac tgatgaggac 550

gagataggag ctgccaaagc cctgatgaga cttcaggaca catacaggct 600

ggaccagggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650

caatgctgag tgtggatgac tgctttggga tgggccgctc ggctacaat 700

gaaggggact attatcatat ggtgttgtgg atggagcagg tgctaaagca 750

gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800

acctcagcta tgctgtcttc cagttgggtg atctgcaccg tgccttgag 850

ctcacccgcc gcctgctctc ccttgacca agccacgaac gagctggagg 900
 gaatctgcgg tactttgagc agttattgga ggaagagaga gaaaaaacgt 950
 taacaaatca gacagaagct gagctagcaa cccagaagg catctatgag 1000
 aggcctgtgg actacctgcc tgagagggat gtttacgaga gcctctgtcg 1050
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 gaggaggacg agtgggacag cccgcacatc gtcaggact acgatgtcat 1200
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 cacgagccac cgttcgtgat cccaagacag gagtcctcac tgtcgccagc 1300
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 ggcccgagta aatcgtcgga tgcagcatat cacagggtta acagtaaaga 1400
 ctgcagaatt gttacaggtt gcaaattatg gagtgggagg acagtatgaa 1450
 ccgcacttcg acttctctag gcgacctttt gacagcggcc taaaacaga 1500
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 accatactag ggcgactcct gtgtgactga agtcccagcc cttccattca 1950
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 gtgtgagatg tttcagtga ccaaagttct gataccttgt ttacatgttt 2100
 gtttttatgg catttctatc tattgtggct ttacaaaaa ataaaatgtc 2150
 cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met	Lys	Leu	Trp	Val	Ser	Ala	Leu	Leu	Met	Ala	Trp	Phe	Gly	Val
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Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met
				20					25					30
Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Lys	Glu	Leu	Val	Gln	Ser	Leu	Lys
				35					40					45
Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser
				50					55					60
Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp
				65					70					75
Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val
				80					85					90
Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu
				95					100					105
Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg
				110					115					120
Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala
				125					130					135
Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile
				140					145					150
Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser
				155					160					165
Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
				170					175					180
Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln
				185					190					195
Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Thr	Lys	Ser	Gln	Val	Leu
				200					205					210
Asp	Tyr	Leu	Ser	Tyr	Ala	Val	Phe	Gln	Leu	Gly	Asp	Leu	His	Arg
				215					220					225
Ala	Leu	Glu	Leu	Thr	Arg	Arg	Leu	Leu	Ser	Leu	Asp	Pro	Ser	His
				230					235					240
Glu	Arg	Ala	Gly	Gly	Asn	Leu	Arg	Tyr	Phe	Glu	Gln	Leu	Leu	Glu
				245					250					255
Glu	Glu	Arg	Glu	Lys	Thr	Leu	Thr	Asn	Gln	Thr	Glu	Ala	Glu	Leu
				260					265					270

Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro	275	280	285
Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys	290	295	300
Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His	305	310	315
Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu	320	325	330
Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met	335	340	345
Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys	350	355	360
Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr	365	370	375
Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp	380	385	390
Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile	395	400	405
Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn	410	415	420
Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg	425	430	435
Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala	440	445	450
Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr	455	460	465
Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr	470	475	480
Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr	485	490	495
Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp	500	505	510
Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg	515	520	525
Pro Cys Gly Ser Thr Glu Val Asp	530		

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcaciaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 336

acactcagca ttgcctggta cttg 24

<210> 337

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 337

gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338

<211> 2789

<212> DNA

<213> Homo Sapien

<400> 338

gcagtattga gttttacttc ctccctctttt tagtggaaga cagaccataa 50
tcccagtggtg agtgaaattg attgtttcat ttattaccgt tttggctggg 100
ggttagttcc gacaccttca cagttgaaga gcaggcagaa ggagttgtga 150
agacaggaca atcttcttgg ggatgctggg cctggaagcc agcgggcctt 200
gctctgtctt tggcctcatt gaccccaggt tctctgggta aaactgaaag 250
cctactactg gcctgggtgcc catcaatcca ttgatccttg aggctgtgcc 300
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ttggctctgc tgcggccagc gcttcccctc atcttagggc tgtctctggg 400
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atccctgtgt cgaggctgta ggggagcgag gagggccaca gaatccagat 500
tcgagagctc ggctagacca aagtgatgaa gacttcaaac cccggattgt 550
cccctactac agggacccca acaagcccta caagaagggtg ctcaggactc 600
ggtacatcca gacagagctg ggctcccgtg agcgggtgct ggtggctgtc 650
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cccgggctcc agcagggatg cagggtggtg tcatgggga tgagcggccc 800
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aactctacca ccgctgccg ctcagcaacc tggaggggct agggggccgt 2600
gccagctgg ctatggctct ctttgagcag gagcaggcca atagcactta 2650
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tttttaaata tgaaaatgtt attaaacatg tcttctgcc 2789

<210> 339
 <211> 772
 <212> PRT
 <213> Homo Sapien

<400> 339

Met	Arg	Leu	Ser	Ser	Leu	Leu	Ala	Leu	Leu	Arg	Pro	Ala	Leu	Pro	1	5	10	15
Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg	20	25	30	
Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala	35	40	45	
Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg	50	55	60	
Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr	65	70	75	
Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg	80	85	90	
Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala	95	100	105	
Val	Leu	Thr	Ser	Arg	Ala	Thr	Leu	Ser	Thr	Leu	Ala	Val	Ala	Val	110	115	120	
Asn	Arg	Thr	Val	Ala	His	His	Phe	Pro	Arg	Leu	Leu	Tyr	Phe	Thr	125	130	135	
Gly	Gln	Arg	Gly	Ala	Arg	Ala	Pro	Ala	Gly	Met	Gln	Val	Val	Ser	140	145	150	
His	Gly	Asp	Glu	Arg	Pro	Ala	Trp	Leu	Met	Ser	Glu	Thr	Leu	Arg	155	160	165	
His	Leu	His	Thr	His	Phe	Gly	Ala	Asp	Tyr	Asp	Trp	Phe	Phe	Ile	170	175	180	
Met	Gln	Asp	Asp	Thr	Tyr	Val	Gln	Ala	Pro	Arg	Leu	Ala	Ala	Leu	185	190	195	
Ala	Gly	His	Leu	Ser	Ile	Asn	Gln	Asp	Leu	Tyr	Leu	Gly	Arg	Ala	200	205	210	
Glu	Glu	Phe	Ile	Gly	Ala	Gly	Glu	Gln	Ala	Arg	Tyr	Cys	His	Gly	215	220	225	
Gly	Phe	Gly	Tyr	Leu	Leu	Ser	Arg	Ser	Leu	Leu	Leu	Arg	Leu	Arg	230	235	240	
Pro	His	Leu	Asp	Gly	Cys	Arg	Gly	Asp	Ile	Leu	Ser	Ala	Arg	Pro	245	250	255	

Asp	Glu	Trp	Leu	Gly	Arg	Cys	Leu	Ile	Asp	Ser	Leu	Gly	Val	Gly	
				260					265					270	
Cys	Val	Ser	Gln	His	Gln	Gly	Gln	Gln	Tyr	Arg	Ser	Phe	Glu	Leu	
				275					280					285	
Ala	Lys	Asn	Arg	Asp	Pro	Glu	Lys	Glu	Gly	Ser	Ser	Ala	Phe	Leu	
				290					295					300	
Ser	Ala	Phe	Ala	Val	His	Pro	Val	Ser	Glu	Gly	Thr	Leu	Met	Tyr	
				305					310					315	
Arg	Leu	His	Lys	Arg	Phe	Ser	Ala	Leu	Glu	Leu	Glu	Arg	Ala	Tyr	
				320					325					330	
Ser	Glu	Ile	Glu	Gln	Leu	Gln	Ala	Gln	Ile	Arg	Asn	Leu	Thr	Val	
				335					340					345	
Leu	Thr	Pro	Glu	Gly	Glu	Ala	Gly	Leu	Ser	Trp	Pro	Val	Gly	Leu	
				350					355					360	
Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp	
				365					370					375	
Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala	
				380					385					390	
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp	
				395					400					405	
Ala	Leu	Glu	Thr	Ala	Leu	Glu	Gln	Leu	Asn	Arg	Arg	Tyr	Gln	Pro	
				410					415					420	
Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg	
				425					430					435	
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu	
				440					445					450	
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg	
				455					460					465	
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met	
				470					475					480	
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu	
				485					490					495	
Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe	
				500					505					510	
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu	
				515					520					525	
Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp	
				530					535					540	

Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg	
				545						550				555	
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala	
				560					565					570	
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro	
				575					580					585	
Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly	
				590					595					600	
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp	
				605					610					615	
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu	
				620					625					630	
Ser	Pro	Gln	Arg	Ser	Pro	Pro	Gly	Pro	Pro	Gly	Ala	Gly	Pro	Asp	
				635					640					645	
Pro	Pro	Ser	Pro	Pro	Gly	Ala	Asp	Pro	Ser	Arg	Gly	Ala	Pro	Ile	
				650					655					660	
Gly	Gly	Arg	Phe	Asp	Arg	Gln	Ala	Ser	Ala	Glu	Gly	Cys	Phe	Tyr	
				665					670					675	
Asn	Ala	Asp	Tyr	Leu	Ala	Ala	Arg	Ala	Arg	Leu	Ala	Gly	Glu	Leu	
				680					685					690	
Ala	Gly	Gln	Glu	Glu	Glu	Glu	Ala	Leu	Glu	Gly	Leu	Glu	Val	Met	
				695					700					705	
Asp	Val	Phe	Leu	Arg	Phe	Ser	Gly	Leu	His	Leu	Phe	Arg	Ala	Val	
				710					715					720	
Glu	Pro	Gly	Leu	Val	Gln	Lys	Phe	Ser	Leu	Arg	Asp	Cys	Ser	Pro	
				725					730					735	
Arg	Leu	Ser	Glu	Glu	Leu	Tyr	His	Arg	Cys	Arg	Leu	Ser	Asn	Leu	
				740					745					750	
Glu	Gly	Leu	Gly	Gly	Arg	Ala	Gln	Leu	Ala	Met	Ala	Leu	Phe	Glu	
				755					760					765	
Gln	Glu	Gln	Ala	Asn	Ser	Thr									
				770											

<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

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tgtccccaag ccgttctaga cgcgggaaaa atgctttctg aaagcagctc 100

ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150
tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250
ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300
ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350
accaaacact gtgacaaagc agagtctctc agttctgaaa atgttaaagt 400
gtttgagtca attaatatgg acacaaatga catgtgggta atgatgagaa 450
aagcttacia atacgccttt gataagtata gagaccaata caactgggtc 500
ttccttgcac gcccactac gtttgctatc attgaaaacc taaagtattt 550
tttgttaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600
aatctggaga ctttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650
gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700
tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750
cagtttgcct gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800
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gtaactacat atccaatata gctgtatgtt tctttttctt ttctaatttg 1150
gtggcactgg tataaccaca cattaaagtc agtagtacat ttttaaata 1200
gggtgggtttt tttctttaaa acacatgaac attgtaaatg tgttggaag 1250
aagtgtttta agaataataa ttttgcaaata aaactattaa taaatattat 1300
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tttgctgatt ggttaaaaaa ttttaacagg tcttttagcgt tctaagatat 1400
gcaaatgata tctctagttg tgaatttgtg attaaagtaa aacttttagc 1450
tgtgtgttcc ctttacttct aatactgatt tatgttctaa gcctcccaa 1500

gttcgaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550

attaaagtga aagttgaaaa at 1572

<210> 341

<211> 318

<212> PRT

<213> Homo Sapien

<400> 341

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Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile
				20					25					30

Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
				35					40					45

Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
				50					55					60

Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
				65					70					75

Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
				80					85					90

Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
				95					100					105

Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
				110					115					120

Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
				125					130					135

Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
				140					145					150

Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
				155					160					165

Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
				170					175					180

Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
				185					190					195

Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
				200					205					210

Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
				215					220					225

Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
				230					235					240

Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile
245 250 255

Lys Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys
260 265 270

Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln
275 280 285

Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly
290 295 300

His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser
305 310 315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttctagacg cgg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaatgc cctaaggcgg tataacccc 28

<210> 345

<211> 50

<212> DNA

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<220>
<223> Synthetic Oligonucleotide Probe

<400> 345
gggtgtgatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50

<210> 346
<211> 25
<212> DNA
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<400> 346
gggatgcagg tgggtgtctca tgggg 25

<210> 347
<211> 18
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 347
ccctcatgta cgggtcc 18

<210> 348
<211> 48
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<400> 348
ggattctaatac gactcact atagggctca gaaaagcgca acagagaa 48

<210> 349
<211> 47
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<220>
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<400> 349
ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47

<210> 350
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<400> 350
ggattctaatacgcactcactatagggcgccgatgtccactggggctac 48

<210> 351
<211> 48
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 351
ctatgaaattaacccctcactaaagggacgaggaagatgggcggatgggt 48

<210> 352
<211> 47
<212> DNA
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<400> 352
ggattctaatacgcactcactatagggcaccacgcgtccggctgctt 47

<210> 353
<211> 48
<212> DNA
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<220>
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<400> 353
ctatgaaattaacccctcactaaagggacggggacaccacggaccaga 48

<210> 354
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
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<400> 354
ggattctaatacgcactcactatagggcttgctgcggtttttgttcctg 48

<210> 355
<211> 48
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 355

ctatgaaatt aaccctcact aaagggagct gccgatccca ctggtatt 48

<210> 356

<211> 46

<212> DNA

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<220>

<223> Synthetic Oligonucleotide Probe

<400> 356

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<210> 357

<211> 48

<212> DNA

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<220>

<223> Synthetic Oligonucleotide Probe

<400> 357

ctatgaaatt aaccctcact aaagggagcc cgggcatggt ctcagtta 48

<210> 358

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 358

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<210> 359

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

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<400> 359

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<210> 360

<211> 48

<212> DNA

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<220>

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<400> 360

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<210> 361
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<220>
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<400> 361
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<210> 362
<211> 47
<212> DNA
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<220>
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<400> 362
ggattctaatt acgactcact atagggcccg cctcgctcct gctcctg 47

<210> 363
<211> 48
<212> DNA
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<220>
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<400> 363
ctatgaaatt aaccctcact aaagggagga ttgccgac cctcacag 48

<210> 364
<211> 47
<212> DNA
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<220>
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<400> 364
ggattctaatt acgactcact atagggcccc tctgccttc cctgtcc 47

<210> 365
<211> 48
<212> DNA
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<220>
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<400> 365
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<210> 366
<211> 48

<212> DNA
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<220>
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<400> 366
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<210> 367
<211> 47

<212> DNA
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<220>
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<400> 367
ctatgaaatt aaccctcact aaaggacag acggggcaga gggagtg 47

<210> 368
<211> 47
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<220>
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<400> 368
ggattctaatac gactcact atagggccag gaggcgtgag gagaaac 47

<210> 369
<211> 48
<212> DNA
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<220>
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<400> 369
ctatgaaatt aaccctcact aaagggaag acatgtcatc gggagtgg 48

<210> 370
<211> 48
<212> DNA
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<220>
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<400> 370
ggattctaatac gactcact atagggccgg gtggaggtgg aacagaaa 48

<210> 371
<211> 48
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371

ctatgaaatt aaccctcact aaagggacac agacagagcc ccatacgc 48

<210> 372

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372

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<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373

ctatgaaatt aaccctcact aaagggagta aggggatgcc accgagta 48

<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 374

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<210> 375

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 375

ctatgaaatt aaccctcact aaagggatcc caggatgatga ggtccaga 48

<210> 376

<211> 997

<212> DNA

<213> Homo Sapien

<400> 376

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aaaaaatgaa ttcatctaaa tcatctgaaa cacaatgcac agagagagga 150
tgcttctctt cccaaatggt cttatggact gttgctggga tccccatcct 200
atttctcagt gcctgtttca tcaccagatg tgttggtgaca tttcgcatct 250
ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300
ctctcctgct acaattatgg atcagggttca gtcaagaatt gttgtccatt 350
gaactgggaa tatttttcaat ccagctgcta cttcttttct actgacacca 400
tttcctgggc gttaagttta aagaactgct cagccatggg ggctcacctg 450
gtggttatca actcacagga ggagcaggaa ttcctttcct acaagaaacc 500
taaaatgaga gagtttttta ttggactgtc agaccagggt gtcgagggtc 550
agtggcaatg ggtggacggc acacctttga caaagtctct gagcttctgg 600
gatgtagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650
gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700
tcaattatth tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750
ggaaaatctc tttaagaaca gaaggcacia ctcaaattgt taaagaagga 800
agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgctc 850
tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900
taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 997
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<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

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Cys Phe Ser Ser Gln Met Phe Leu Trp Thr Val Ala Gly Ile Pro
                      20                      25                      30

Ile Leu Phe Leu Ser Ala Cys Phe Ile Thr Arg Cys Val Val Thr
                      35                      40                      45

Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro
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	50		55		60
Glu Asn Phe Thr	Glu Leu Ser Cys Tyr	Asn Tyr Gly Ser Gly Ser			
	65	70			75
Val Lys Asn Cys	Cys Pro Leu Asn Trp	Glu Tyr Phe Gln Ser Ser			
	80	85			90
Cys Tyr Phe Phe	Ser Thr Asp Thr Ile	Ser Trp Ala Leu Ser Leu			
	95	100			105
Lys Asn Cys Ser	Ala Met Gly Ala His	Leu Val Val Ile Asn Ser			
	110	115			120
Gln Glu Glu Gln	Glu Phe Leu Ser Tyr	Lys Lys Pro Lys Met Arg			
	125	130			135
Glu Phe Phe Ile	Gly Leu Ser Asp Gln	Val Val Glu Gly Gln Trp			
	140	145			150
Gln Trp Val Asp	Gly Thr Pro Leu Thr	Lys Ser Leu Ser Phe Trp			
	155	160			165
Asp Val Gly Glu	Pro Asn Asn Ile Ala	Thr Leu Glu Asp Cys Ala			
	170	175			180
Thr Met Arg Asp	Ser Ser Asn Pro Arg	Gln Asn Trp Asn Asp Val			
	185	190			195
Thr Cys Phe Leu	Asn Tyr Phe Arg Ile	Cys Glu Met Val Gly Ile			
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Asn Pro Leu Asn	Lys Gly Lys Ser Leu				
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<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

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<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380
<211> 49
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<400> 380
ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg 49

<210> 381
<211> 26
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<220>
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<400> 381
gcagattttg aggacagcca cctcca 26

<210> 382
<211> 18
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<213> Artificial Sequence

<220>
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<400> 382
ggccttgag acaaccgt 18

<210> 383
<211> 21
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<220>
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<400> 383
cagactgagg gagatccgag a 21

<210> 384
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 384
cagctgccct tccccaacca 20

<210> 385
<211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 385
catcaagcgc ctctacca 18

<210> 386
<211> 21
<212> DNA
<213> Artificial Sequence

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<400> 386
cacaaactcg aactgcttct g 21

<210> 387
<211> 18
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<213> Artificial Sequence

<220>
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<400> 387
gggccatcac agctccct 18

<210> 388
<211> 22
<212> DNA
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<220>
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<400> 388
gggatgtggt gaacacagaa ca 22

<210> 389
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
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<400> 389
tgccagctgc atgctgccag tt 22

<210> 390
<211> 20
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<400> 390

cagaaggatg tcccgtggaa 20

<210> 391

<211> 17

<212> DNA

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<210> 392

<211> 21

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<400> 392

gacggcatcc tcaggccac a 21

<210> 393

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

atgtcctcca tgcccacgcg 20

<210> 394

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<212> DNA

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<220>

<223> Synthetic oligonucleotide probe

<400> 394

gagtgcgaca tcgagagctt 20

<210> 395

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
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<400> 395
ccgcagcctc agtgatga 18

<210> 396
<211> 21
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<400> 396
gaagagcaca gctgcagatc c 21

<210> 397
<211> 22
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<400> 397
gaggtgtcct ggctttggta gt 22

<210> 398
<211> 20
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cctctggcgc cccactcaa 20

<210> 399
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<400> 399
ccaggagagc tggcgatg 18

<210> 400
<211> 23
<212> DNA
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<220>
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<400> 400
gcaaattcag ggctcactag aga 23

<210> 401
<211> 29
<212> DNA
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<400> 401
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<210> 402
<211> 22
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<400> 402
ggcagagact tccagtcact ga 22

<210> 403
<211> 22
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<220>
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<400> 403
gccaaaggtg gtgtagata gg 22

<210> 404
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<212> DNA
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<220>
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caggccccct tgatctgtac ccca 24

<210> 405
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<220>
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<400> 405

gggacgtgct tctacaagaa cag 23

<210> 406
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<220>
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<213> Homo Sapien

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